

J8/226248

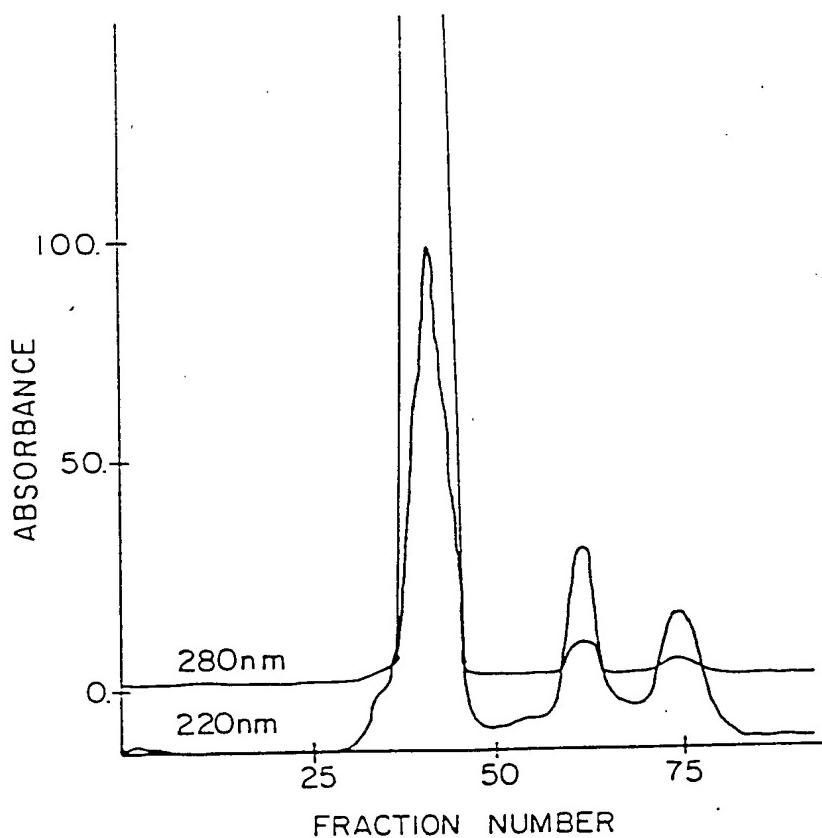


Fig. 1a

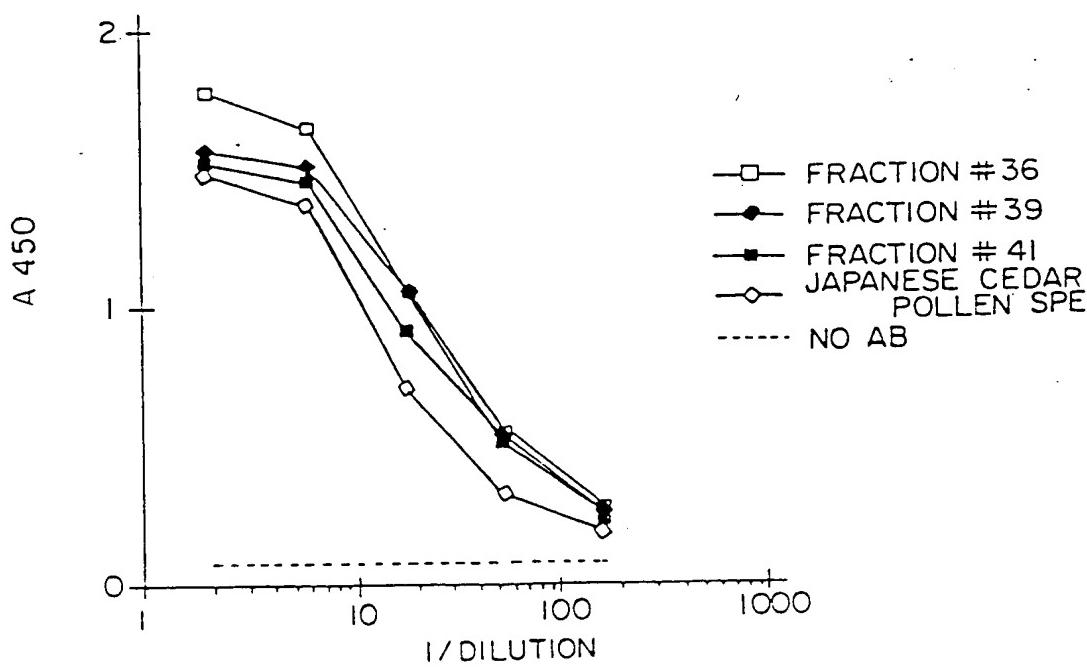


Fig. 3

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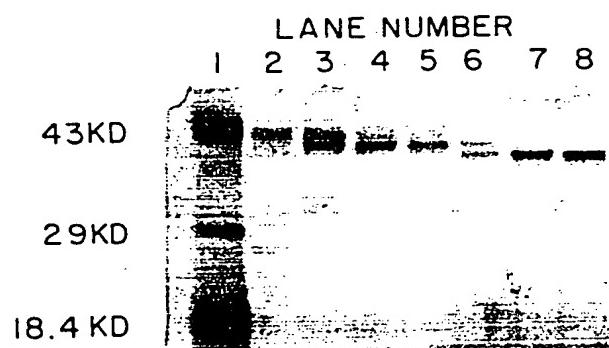


Fig. 1b

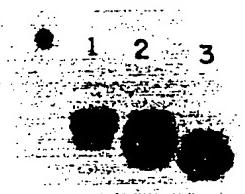


Fig. 2

5' -AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACCA 60

AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT 107
 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
 -21 -20 -15 -10

GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA 155
 Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
 -5 1 5

GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA 203
 Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
 10 15 20 25

GTC GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GAT CTT TAT 251
 Val Gly Phe Gly Ser Ser Thr Met Gly Lys GLY GLY Asp Leu Tyr
 30 35 40

ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT 299
 Thr Val Thr Asn Ser Asp Asp Pro Val Asn Pro Ala Pro Gly Thr
 45 50 55

CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT 347
 Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser
 60 65 70

Fig. 4

GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATT GCT ATT GGG TAT	395
Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr	
80	
85	
 AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT	443
Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile GLY Asn GLY GLY	
90	
95	
 CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG	491
Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His GLY Leu	
100	
105	
 TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC	539
Tyr Leu Tyr GLY Cys Ser Thr Ser Val Leu GLY Asn Val Leu Ile Asn	
110	
115	
 GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT	587
Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp GLY Asp Ala Leu	
120	
125	
130	
135	
 ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC	635
Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser	
140	
145	
150	
155	
160	
165	

Fig. 4 cont.

AAT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT	683	
Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val		
175	180	
ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA	731	
Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu		
190	195	200
GGG CAT GAT GCA TAT AGT GAT GAC AAA TCC ATG AAG GTG ACA GTG	779	
Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val		
205	210	215
GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA	827	
Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala		
220	225	230
CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT GAC CCA TGG ACT	875	
Arg Tyr Gly Leu Val His Val Ala Asn Asn Tyr Asp Pro Trp Thr		
235	240	245
ATA TAT GCA ATT GGT GGG AGT TCA AAT CCA ACC ATT CTA AGT GAA GGG	923	
Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly		
250	255	260
		265

Fig. 4 cont.

971

AAT AGT TTC ACT GCA CCA AAT GAG AGC TAC AAG CAA GTA ACC ATA
 Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile
 270 275 280

1019

CGT ATT GGA TGC AAA ACA TCA TCA TCT TGT TCA AAT TGG GTG TGG CAA
 Arg Ile GLY CYS Lys Thr Ser Ser Cys Ser Asn Trp Val Trp Gln
 285 290 295

1067

TCT ACA CAA GAT GTT TTT TAT GGA GCT TAT TTT GTA TCA TCA GGG
 Ser Thr Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly
 300 305 310

1115

AAA TAT GAA GGG GGT AAT ATA TAC ACA AAG AAA GAA GCT TTC AAT GTT
 Lys Tyr Glu GLY Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val
 315 320 325

1163

GAG AAT GGG AAT GCA ACT CCT CAA TTG ACA AAA AAT GCT GGG GTT TTA
 Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu
 330 335 340 345

1217

ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCCA TATATTCTAG CATGTTGTAC
 Thr Cys Ser Leu Ser Lys Arg Cys
 350

1277

TATCTAAATT AACATCAACA AGAAAATAA TCATGATGTA TATTGTTGTA TTGATGTCAA

1337

AATAAAAATG TATCTTTAC TATTAATAA AAAAATGATC GATCGGACGG TACCTCTAGA-3'

Fig. 4 cont.

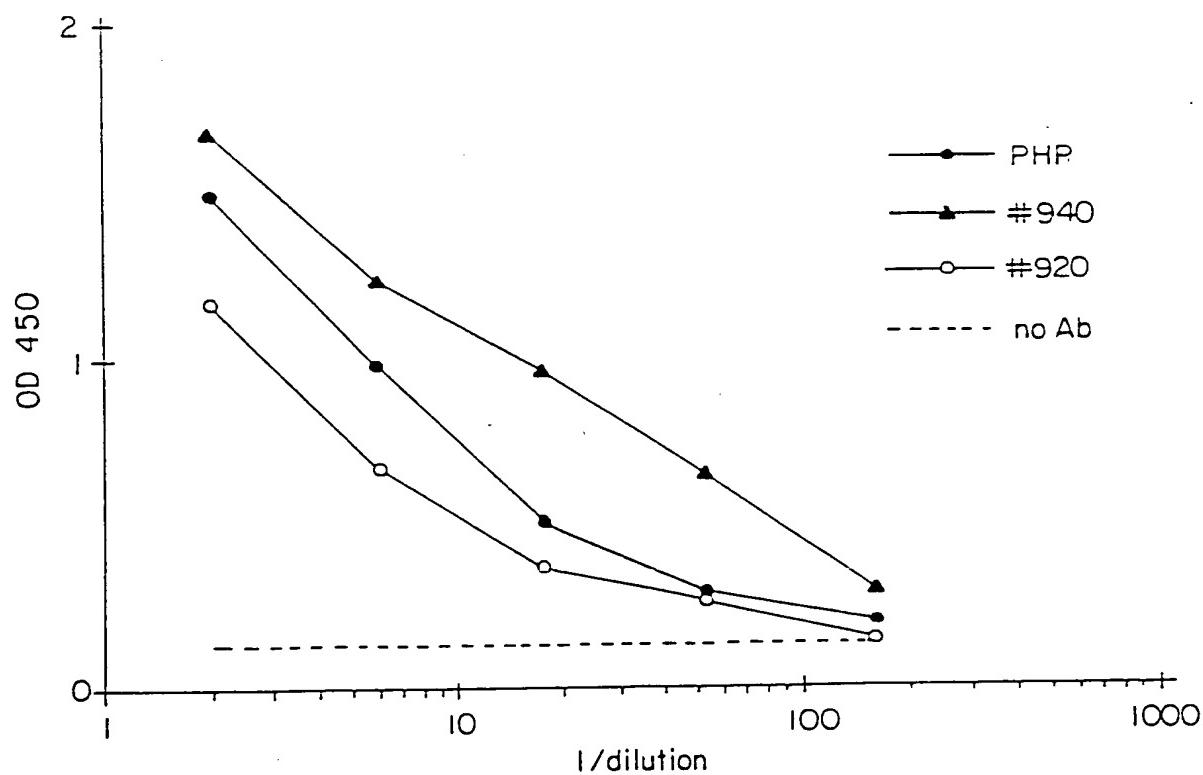


Fig. 5a

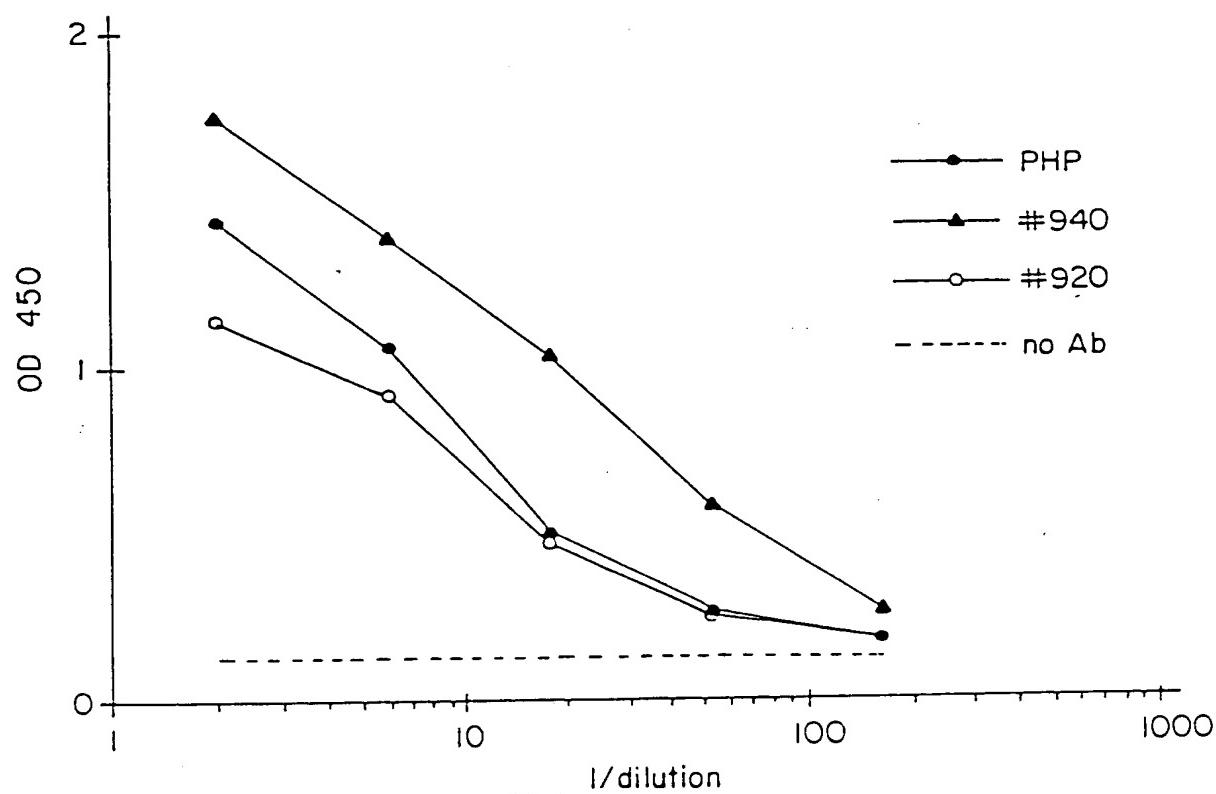
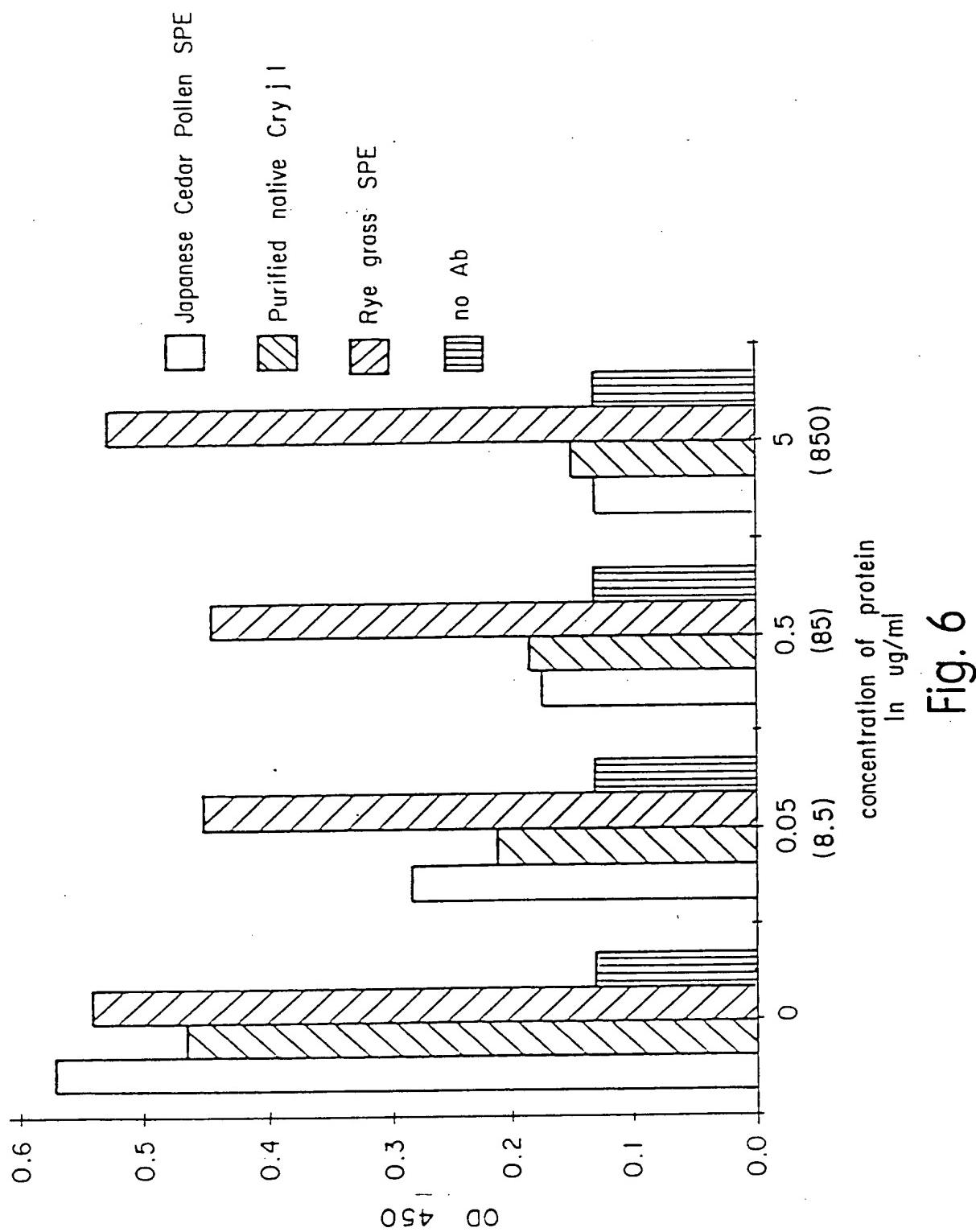


Fig. 5b



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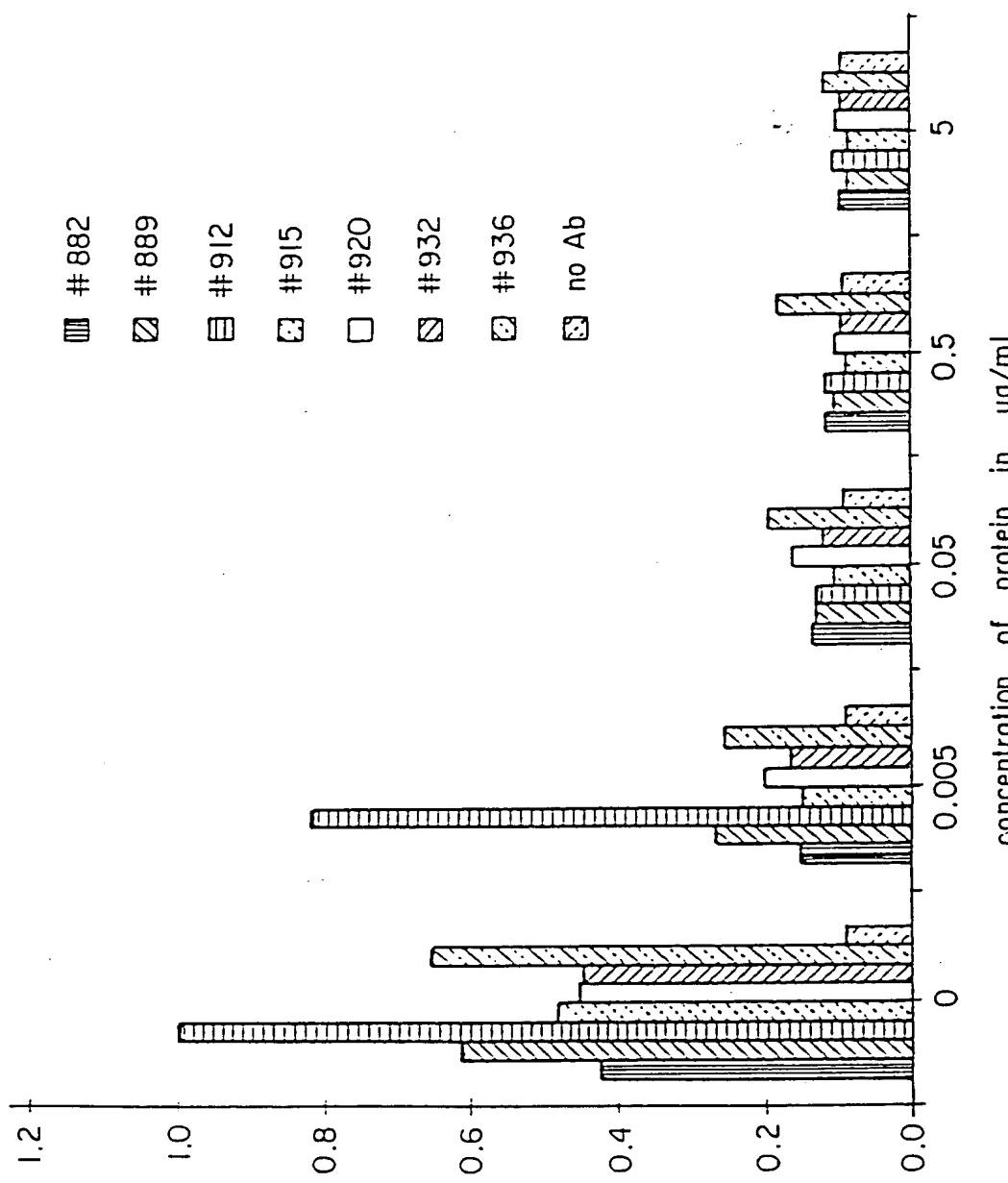


Fig. 7

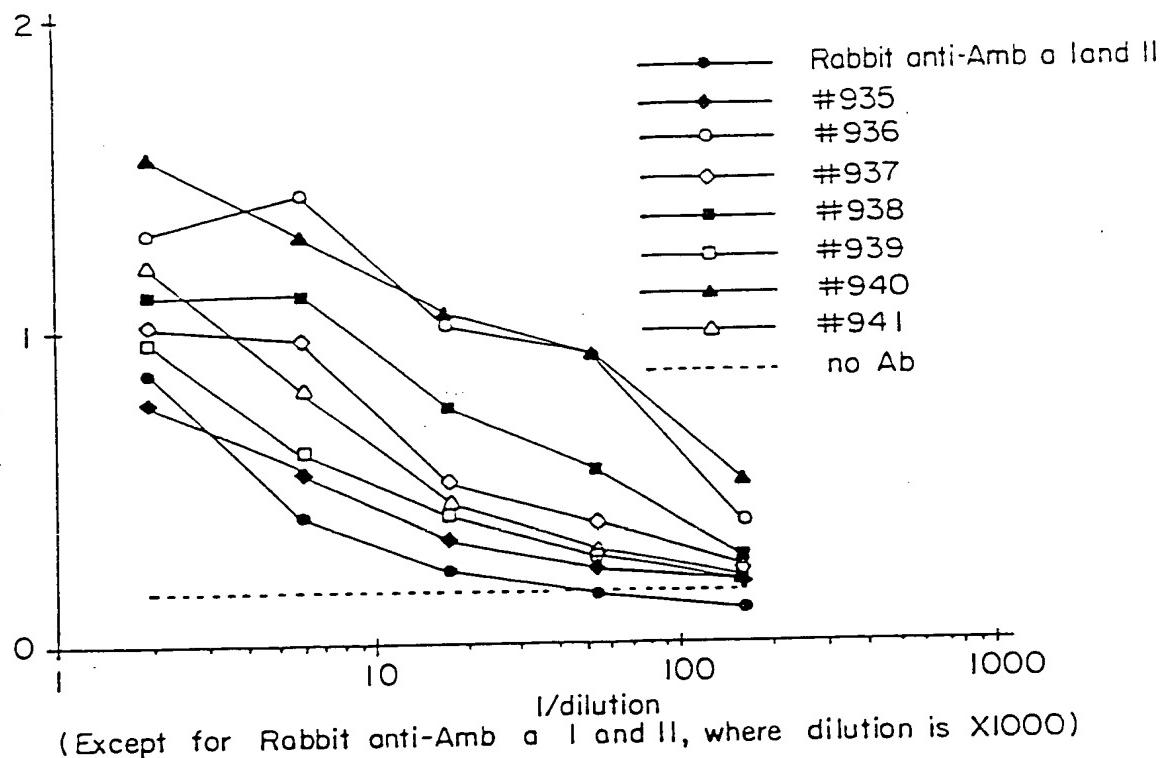


Fig. 8a

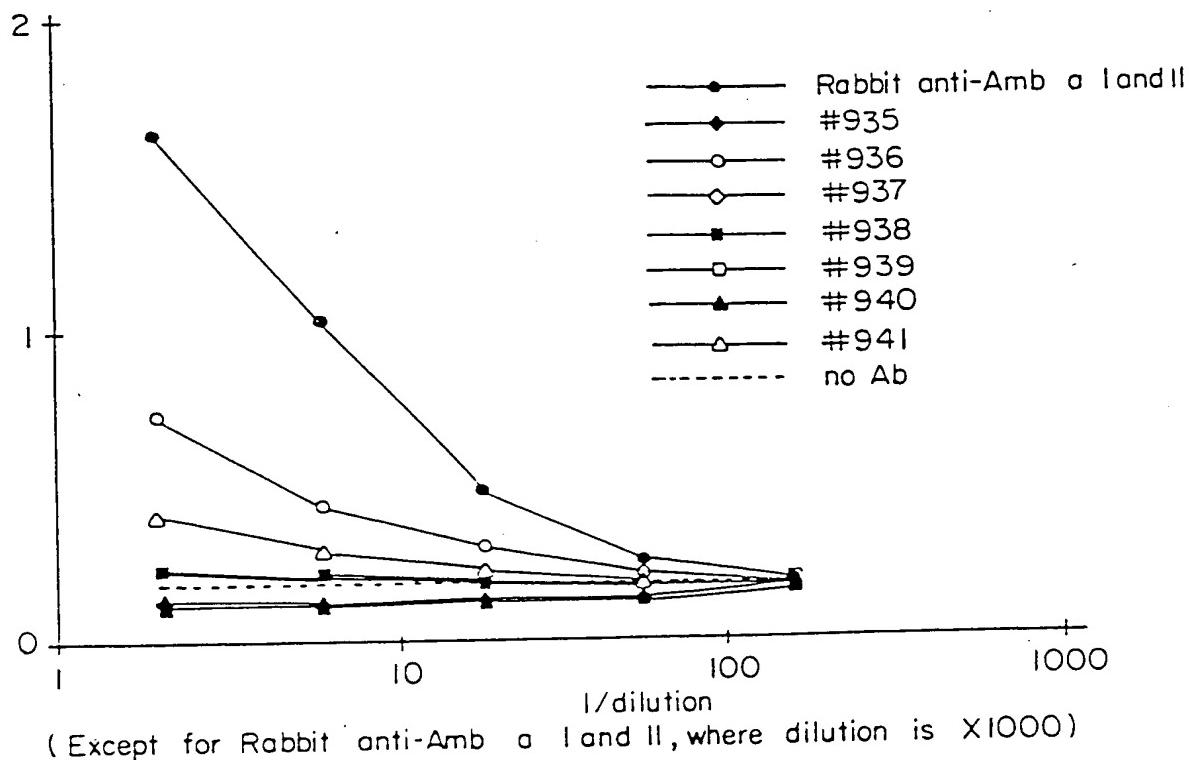
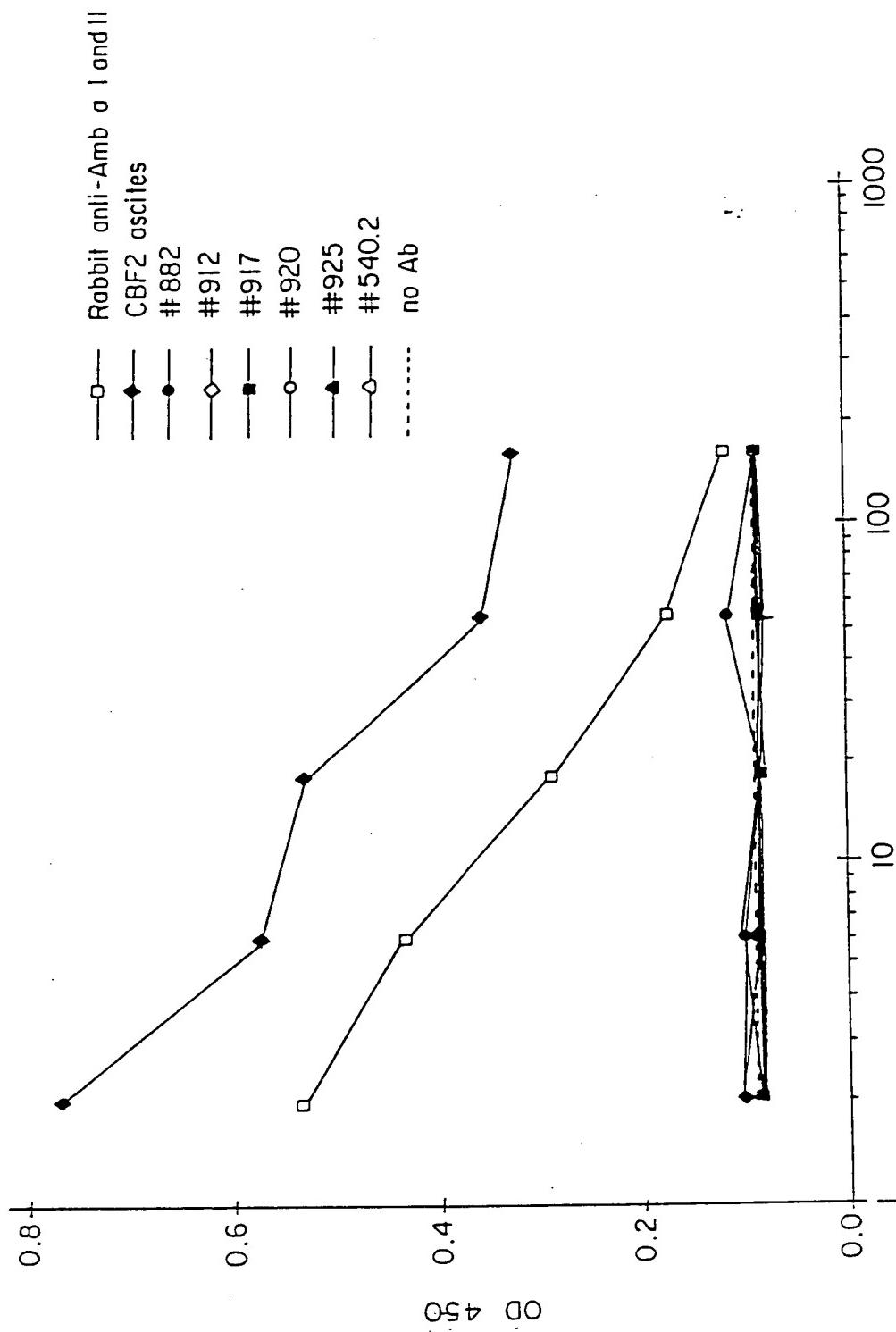


Fig. 8b



(Except for CBF2 and Rabbit anti-Amb α I and II, where dilution is ×1000)

Fig. 9

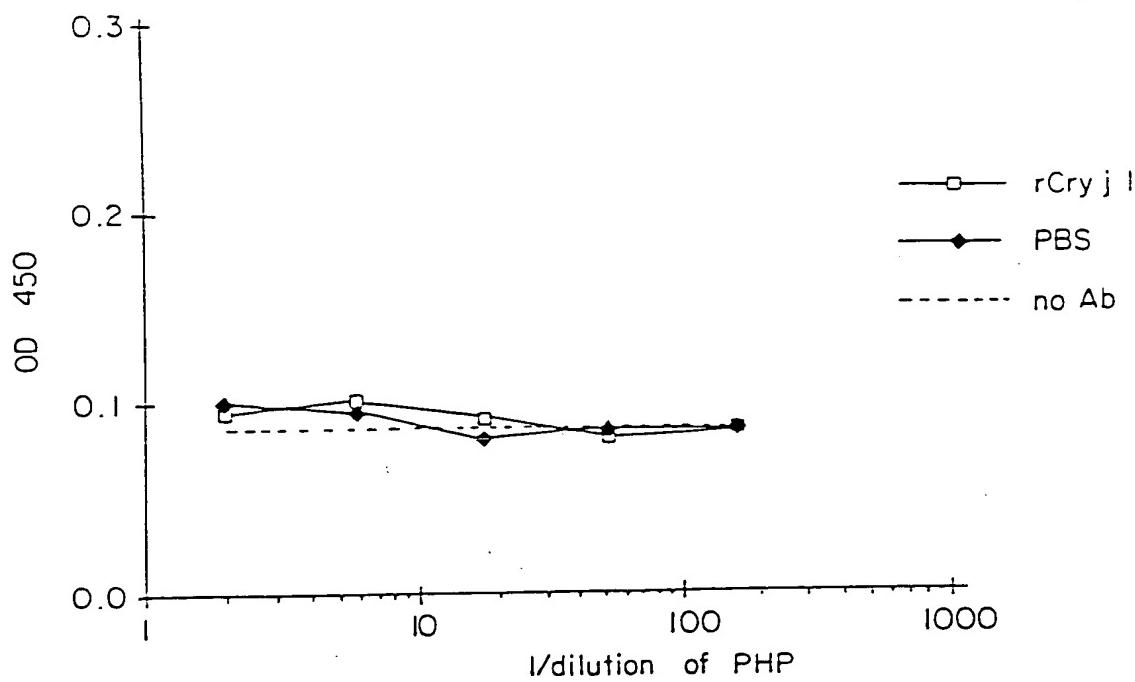


Fig. 10a

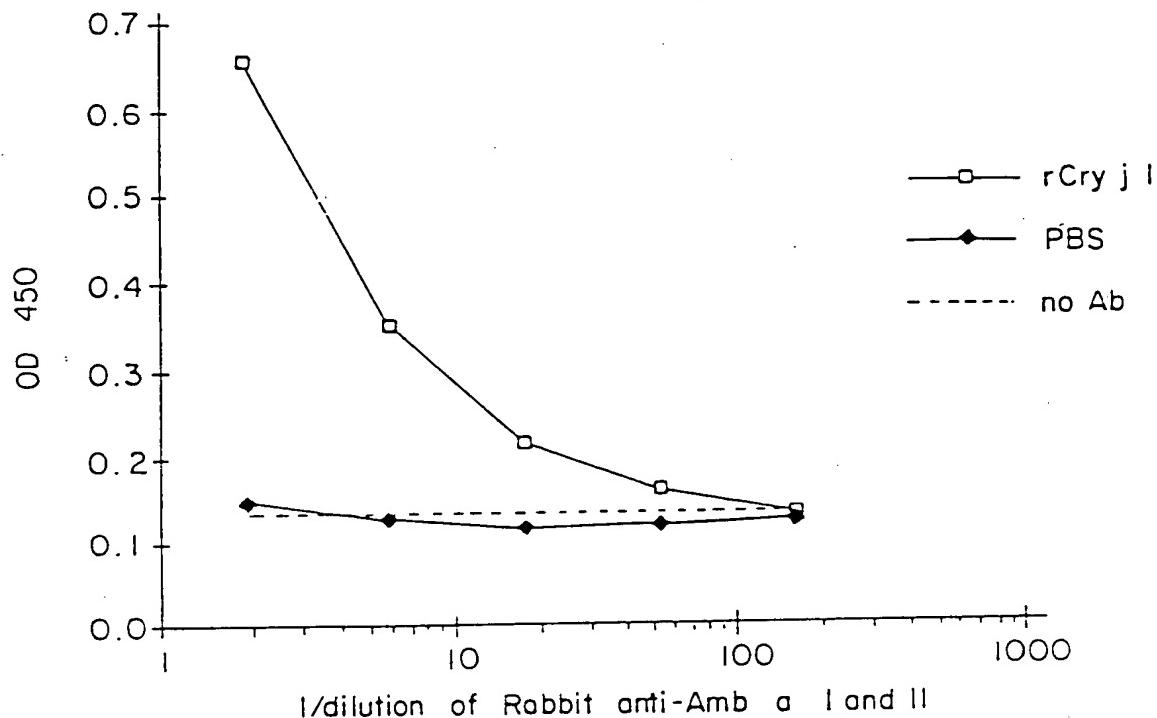


Fig. 10b

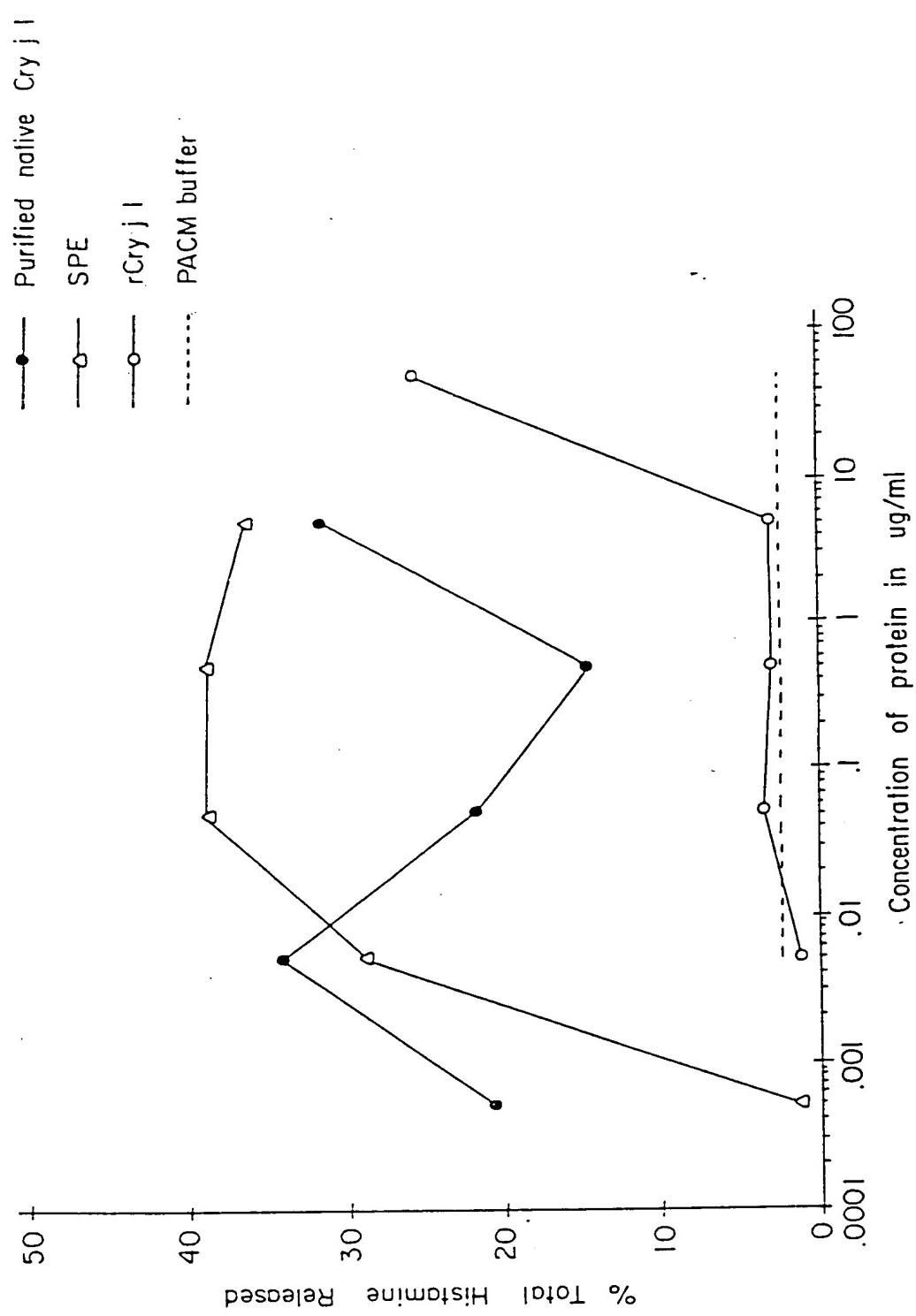


Fig. 11

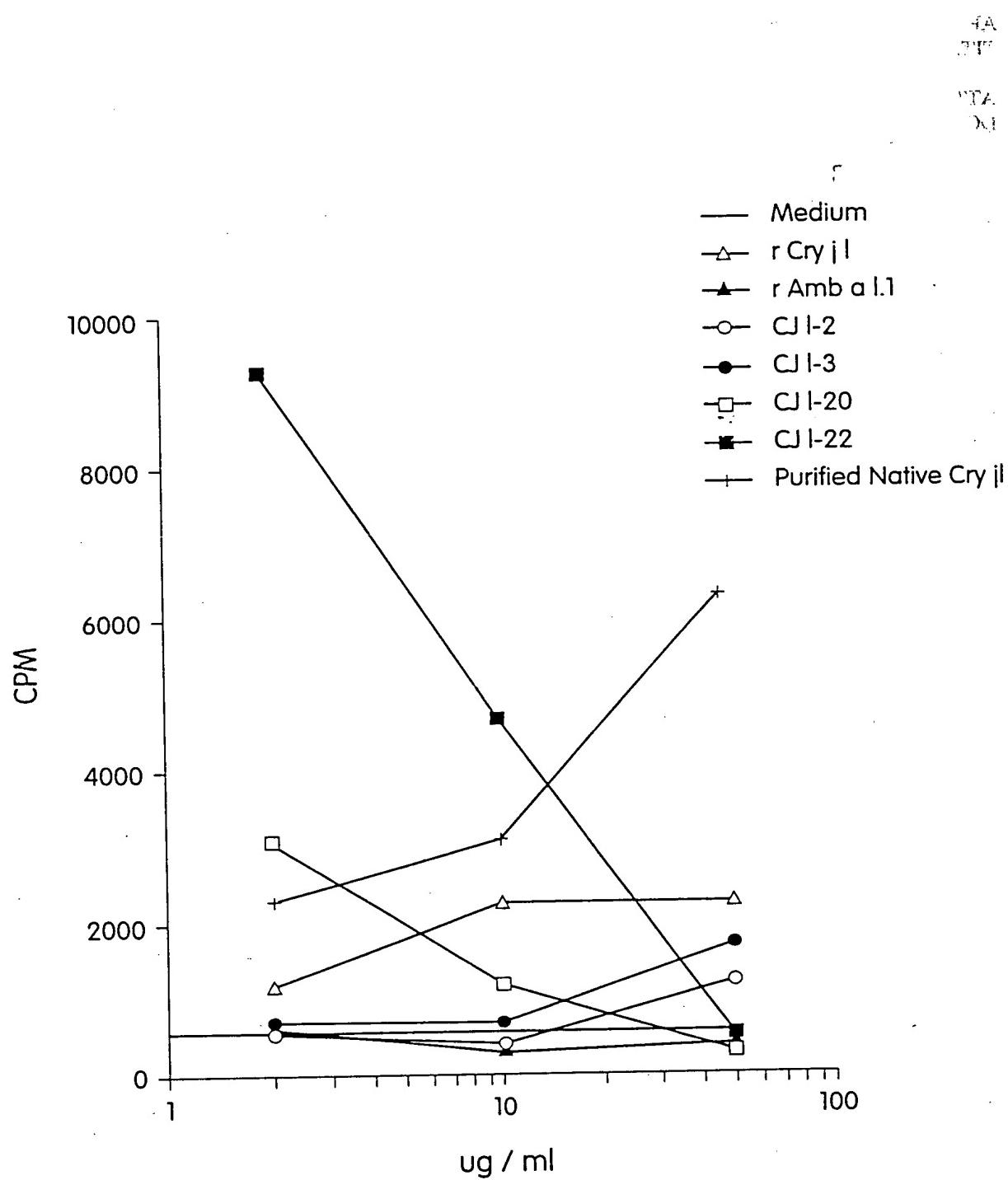


Fig. 12

PEPTIDE NAME

CJI-1 (1-20)	DNPIDSCWRGDSNWAQNRMK
CJI-2 (11-30)	DSNWAQNRMKLADCAVGFGS
CJI-3 (21-40)	LADCAVGFGSSTMGGKGGLD
CJI-4 (31-50)	STMGGKGGLDLYTVTNSDDDP
CJI-5 (41-60)	YTVTNSDDDPVNPAAPGTLRY
CJI-6 (51-70)	VNPAPGTLRYGATRDRPLWI
CJI-7 (61-80)	GATRDRPLWIIIFSGNMNIKL
CJI-8 (71-90)	IFSGNMNIKLKMPMYIAGYK
CJI-9 (81-100)	KMPMYIAGYKTFDGRGAQVY
CJI-10 (91-110)	TFDGRGAQVYIGNGGPCVFI
CJI-11 (101-120)	IGNGGPCVFIRVSNVIIHG
CJI-12 (111-130)	KRVSNVIIHGLYLYGCSTSV
CJI-13 (121-140)	LYLYGCSTSVLGNVLINESF
CJI-14 (131-150)	LGNVLINESFGVEPVHPQDG
CJI-15 (141-160)	GVEPVHPQDGDACTLRTATN
CJI-16 (151-170)	DALTLRTATNIWIDHNSFSN
CJI-17 (161-180)	IWIDHNSFSNSSDGLVDVTL
CJI-18 (171-190)	SSDGLVDVTLTSTGVTISNN
CJI-19 (181-200)	TSTGVTISNNLFFNHHKVML
CJI-20 (191-210)	LFFNHHKVMLLGHDAYSD
CJI-21 (201-220)	LGHDDAYSDDKSMKVTVAFN
CJI-22 (211-230)	KSMKVTVAFNQFGPNCQRM
CJI-23 (221-240)	QFGPNCGQRMPRARGLVHV
CJI-24 (231-250)	PRARYGLVHVANNYDPWTI
CJI-25 (241-260)	ANNYDPWTIYAIGGSSNPT
CJI-26 (251-270)	YAIGGSSNPTILSEGNSFTA
CJI-27 (261-280)	ILSEGNSFTAPNESYKKQVT
CJI-28 (271-290)	PNESYKKQVTIRIGCKTSSS
CJI-29 (281-300)	IRIGCKTSSCSNWVWQSTQ
CJI-30 (291-310)	CSNWVWQSTQDVFYNGAYFV
CJI-31 (301-320)	DVFYNGAYFVSSGKYEGGNI
CJI-32 (311-330)	SSGKYEGGANIYTKKEAFNVE
CJI-33 (321-340)	YTKKEAFNVENGNAATPQLTK
CJI-34 (331-350)	NGNATPQLTKNAGVLTCSLS
CJI-35 (341-353)	NAGVLTCSLSKRC

Fig. 13

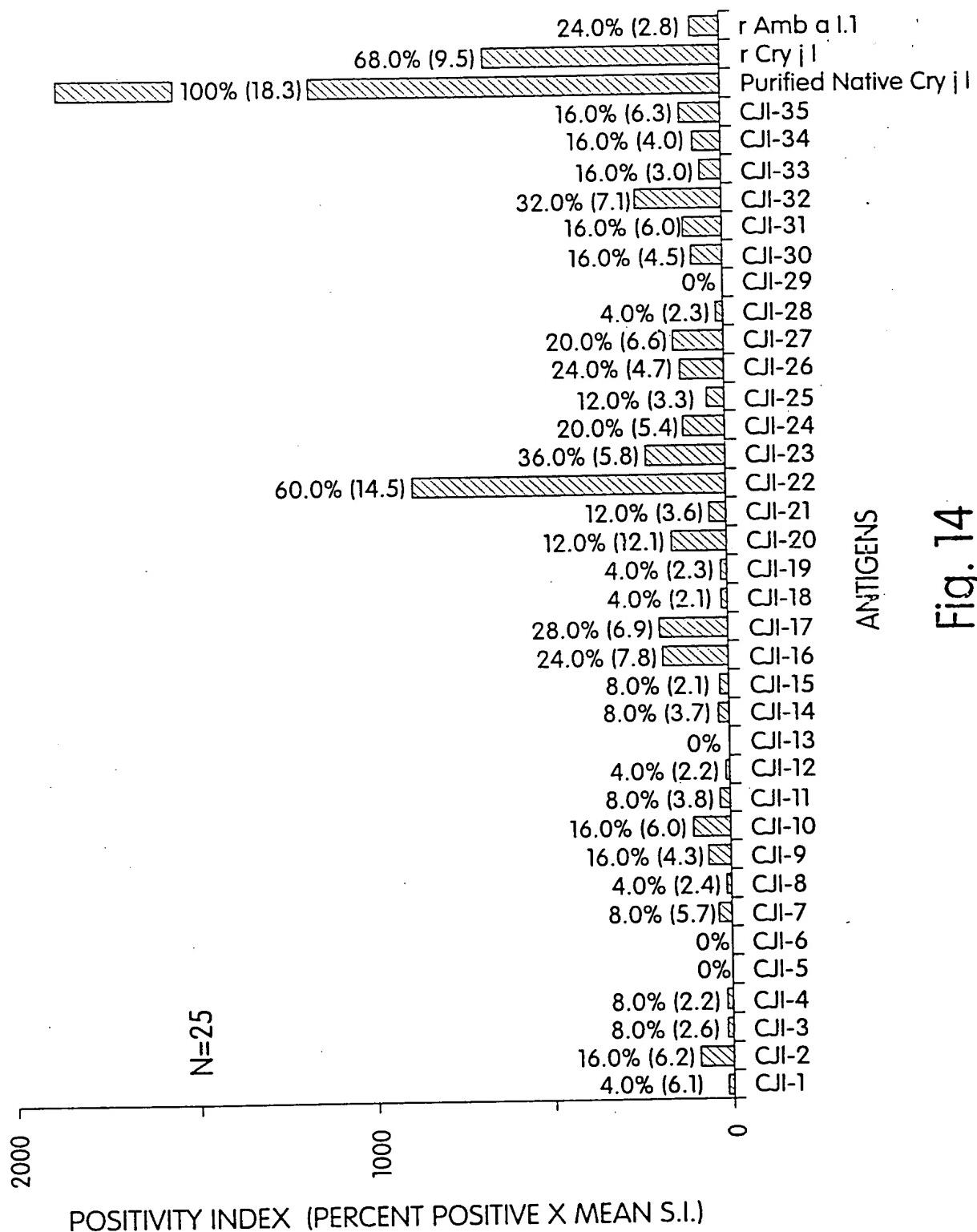


Fig. 14

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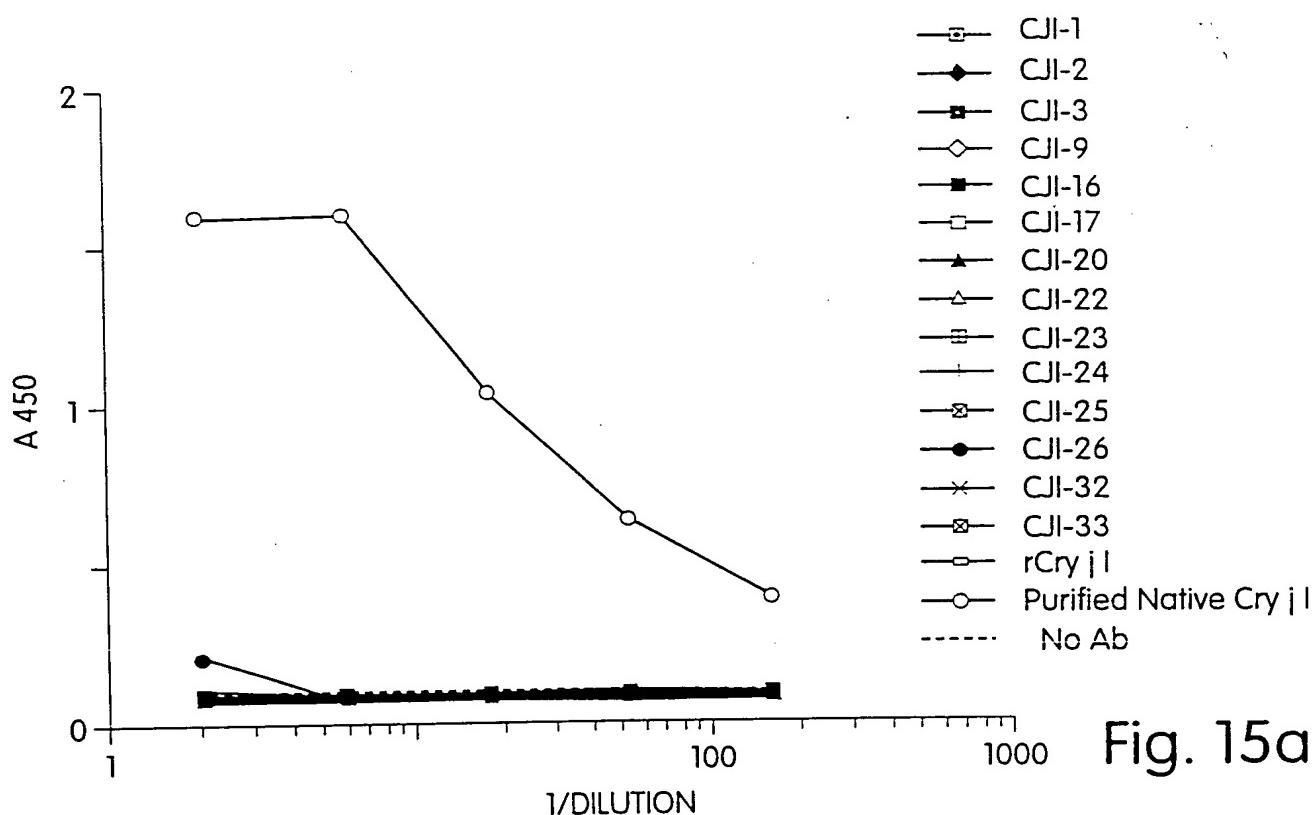


Fig. 15a

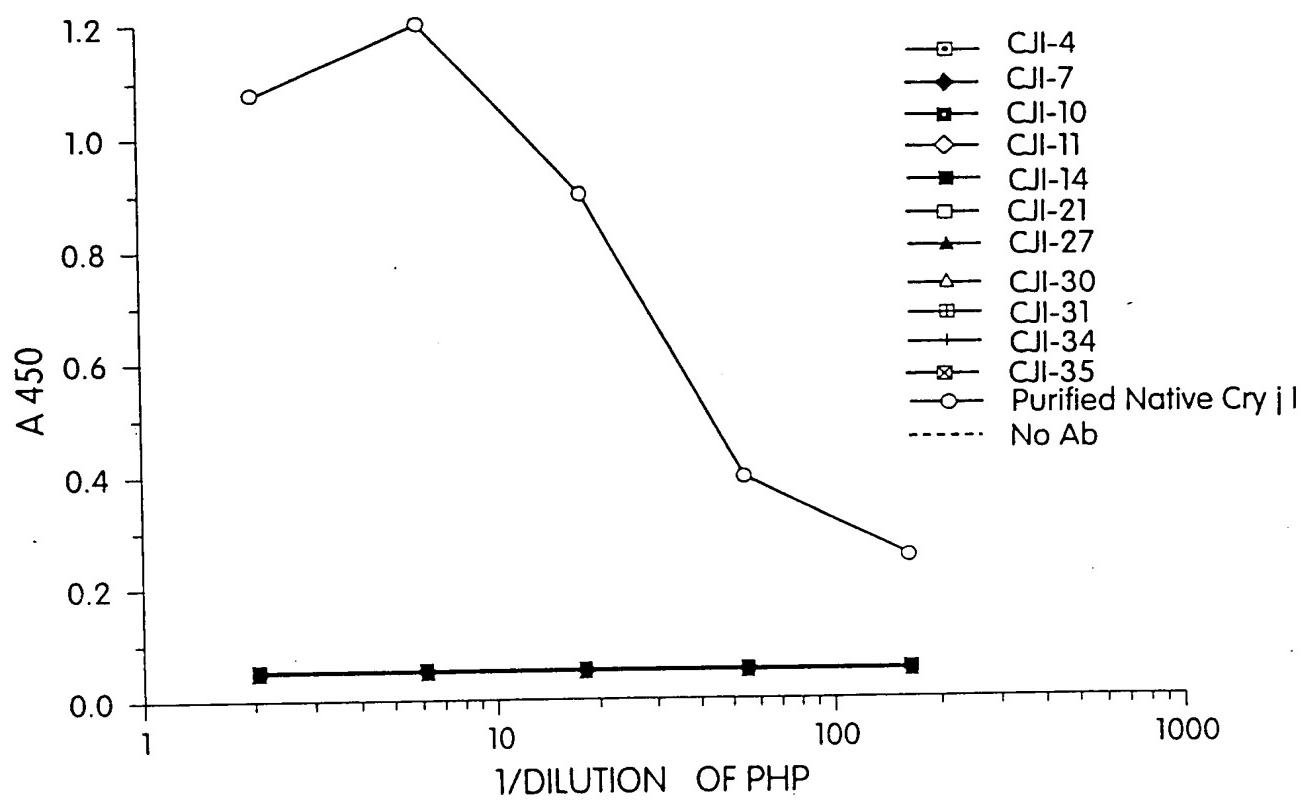


Fig. 15b

5' - AAATTCTTATTCGAAACCTTAAATAAGCCTTCCCATGGCTTCTGTTAATTAGCAGTCCTTGTTT 60

M	A	S	P	C	L	I	A	V	L	V	F
-21	-20				-15				-10		

CCTTTGTGCAATTGTATCTTGTACTCTGATAATCCCATCGACAGCTGGAGAGGAGA 120

L	C	A	I	V	S	C	Y	S	D	N	P	I	D	S	C	W	R	G	D
													+1						
														5					10

TTCGAACTGGATCAAACAGAAATGAAGCTCGCAGACTGTGGCTGTGGGATTGGAAAGCTC 180

S	N	W	D	Q	N	R	M	K	L	A	D	C	A	V	G	F	G	S	S
														20		25			30

CACCATGGGCAAAAGGAGGAGATTACACCGGTACACAAGCACAGATGATAATTCCCTGT 240

T	M	G	G	K	G	G	D	F	Y	T	V	T	S	T	D	D	N	P	V
														40		45			50

GAATCCTACACCAGGAACCTTGTGGCTATGGAGCAACAAGAGAAAAAGCACTTTGGATCAT 300

N	P	T	P	G	T	L	R	Y	G	A	T	R	E	K	A	L	W	I	I
														35		40			55

TTTCTCTCAGAATATGAATATAAGCTCAAGATGCCCTTGTATGTTGCTGGACATAAGAC 360

F	S	Q	N	M	N	I	K	L	K	M	P	L	Y	V	A	G	H	K	T
														75		80		85	90

TATTGACGGCAGGGGAGGAGATGTTCATCTTGGCAACGGGGTCCCCCTGTCTGTTATGAG 420

I	D	G	R	G	A	D	V	H	L	G	N	G	P	C	L	F	M	R	
														95		100		105	110

Fig. 16

GAAAGTGGCCATGTTATTCTCCATAGTTGCATATAACACGGTTGTAATACTGAGTGT	480
K V S H V I L H S L H I H G C N T S V L	
115 120 125 130	
GGGGATGTTGGTAAGTGAGTCTATTGGGGTCAGGCCATGCTCAGGATGGGA	540
G D V L V S E S I G V E P V H A Q D G D	
135 140 145 150	
CGCCATTACTATGCCCATGTTACAAATGCTTGGATTGATCATAATTCTCTCCGATTG	600
A I T M R H V T N A W I D H N S L S D C	
155 160 165 170	
TCTGATGGTCTATCGATGTTACGCTGGCTCCACTGGAAATTACTATCTCCAACATCA	660
S D G L I D V T L G S T G I T I S N N H	
175 180 185 190	
CTTCCTAACCATATAAAGTGGATTAGGACATGATGACATATGACCGATGACAA	720
F F N H H K V M L L G H D D T Y D D K	
195 200 205 210	
ATCTATGAAAGTGACAGTGGCGTTCAATCAATTGGACCTAATGCTGGCAAAGAATGCC	780
S M K V T V A F N Q F G P N A G Q R M P	
215 220 225 230	

Fig. 16 cont.

AAGGGCACGATATGGACTTGTACATGTTGCAAACAATAATTGATCCATGGAAATATA 840
 R A R Y G L V H V A N N N Y D P W N I Y
 235 240 245 250

TGCTTATTGGGAGTTCAAACCAATTCTGAGTGAAAGGGAAATAGTTTCACTGCCCC 900
 A I G G S S N P T I L S E G N S F T A P
 255 260 265 270

AAGTGAGACTTACAAGGAAGCAAGTAACAAAGCGTATAGGGTGTGAATCACCATCAGCTTG 960
 S E S Y K K Q V T K R I G C E S P S A C
 275 280 285 290

TGGGAACGGGTGGAGATCTACACGAGATGCTTTATTAAATGGAGCTTATTGTATC 1020
 A N W V W R S T R D A F I N G A Y F V S
 295 300 305 310

ATCGGGAAACTGAAGAGACCAATATACAAATAGTAATGAAAGCTTCAAAGTTGAGAA 1080
 S G K T E E T N I Y N S N E A F K V E N
 315 320 325 330

TGGGAATGCAGCTCCTCAATTAAACCAAAAATGCTGGAGTTGTAACCTAAGCTCTCTAA 1140
 G N A A P Q L T K N A G V V T -
 335 340 345

ATCTTGCTTATGAAACGAAAAATATATAG-3' 1170

Fig. 16 cont.

226248

'-CGGTATAGATTCTTCTGAGCCCTAAATAATGGCTTCCCCATGCTTAATAAGCAT										60
M	A	S	P	C	L	I	A			
-21	-20							-15		
TCCTTGTTCCTTGTGCAAATTGTATCTTGTCTGATAATCCCATAAGACAGCTTGCT										120
F	L	V	F	L	C	A	I	V	S	C
-10					-5					+1
										5
GGAGGGAGATTGAAACTGGGGTCAAAACAGAAATGAAGGCTCGCAGATTGCCTGGGAT										180
W	R	G	D	S	N	W	G	Q	N	R
10					15					20
										25
TTGGAAGCTCCACCATTACACCAGGAACCTGGGAGGGCAAAGGAGGAGATTTTACACCGTCAACAAGGGCAGATG										240
F	G	S	S	T	M	G	G	K	G	D
30										40
										45
ATAATCCTGTGAATCCTACACCAGGAACCTGGGAGGGCAAAGGAGAACAAGGAGAAAAAGCAC										300
D	N	P	V	N	P	T	P	G	T	L
50										60
										65
TTTGGATCATTCTCTCAGAATATGAATAAGCTCAAGATGCCCTTGTATGTTGCTG										360
L	W	I	I	F	S	Q	N	M	N	I
70										80
										85
GACATAAGACTTATTGACGGCAGGGGAGGAGATGTTCATCTTGGCAACGGGGTCCCTGTC										420
G	H	K	T	I	D	G	R	G	A	D
90										95
										100
										105

Fig. 17

TGTTTATGAGGAAGTGAGCCATGTTATTCTCCATGGTTGCATAACACGGTTGTAATA	480
L F M R K V S H V I L H G L H I H G C N	
110 115 120 125	
CTAGTGTGTTGGGGATGTTGGTAAGTGAGTCTATTGGGGTGGCTGTACACCCCC	540
T S V L G D V L V S E S I G V V P V H P	
130 135 140 145	
AGGACGGAGATGCGTTACTGTGAGGACCTCTGAACATATTGGGTCGACCATAACTC	600
Q D G D A F T V R T S E H I W V D H N T	
150 155 160 165	
TCTCCAATGGCACCGACGCCCTCGGTGACGGTTACTCTTGCTTGTTACTTCT	660
L S N G T D G L V D V T L A S T A V T I	
170 175 180 185	
CCAATACCACTTCTCGACCATGATGAAGTGTGTTAGGACATAGTGATTCAATTCT	720
S N N H F F D H D E V M L L G H S D S F	
190 195 200 205	
CAGATGATAAAGTGTGAAAGTCACAGTGCATTAAACCACTTGGACCTAATTGTGTGC	780
S D D K V M K V T V A F N H F G P N C V	
210 215 220 225	
AACGATGCCAAGGGCTAGATATGGACACTTCAATGTTGAGCCAT	840
Q R L P R A R Y G H F H V V N N N Y E P	
230 235 240 245	

Fig. 17 cont.

GGGGAAATAATGCCATTGGAGGAAGTTCTGATCCAAACATTATAAGTGAAGGGAATAGAT
 W G K Y A I G G S D P T I I S E G N R
 250 255 260 265

TTCCTGCACCAAATGAATCTTATAAAAAGGAGGTGACAATACCGTGTAGGTTGTAATCTA
 F L A P N E S Y K K E V T I R V G C K S
 270 275 280 285

CAAGTTGTGATGCCATTGGAGTCAAAGATGATGCCCTTCCTTAATGGTGCCTATT
 T S C D A W E W R S K D D A F L N G A Y
 290 295 300 305

TTGTACAATCAGGCCAAGGGGTATAATTGGTGGAGGCCATTCAAGGTTGAAAGTGCCTATG
 F V Q S G K G Y N G G E A F K V E S A N
 310 315 320 325

AGGTGCCAACATTGACTAAACATGCTGGAGCATTAAATGTTACCTACCAAACAAATGTG
 E V P T L T K H A G A L K C I P T K Q C
 330 335 340 345

TGATATGAAAAGTCATCGATAATAATGTTGTAATATTTCAGCTTGAATAT
 V I -

GTATAGAAAAGAATTCAACAAATGACACTATTATAATAATTCTTAGTTTATTAA
 GTTGGTATTAAAAAAA-3

1278

Fig. 17 cont.

CJI-41 KMPMYIAGYKTFDGRGAQVYIGNGGPCVFI
 CJI-41.1 PMYIAGYKTFDGRGAQVYIGNGGP
 CJI-41.2 YIAGYKTFDGRGAQVYIGNGGP
 CJI-41.3 KKYIAGYKTFDGRGAQVYIGNGGP

CJI-42 DALTLRTATNIWIDHNSFSNSSDGLVDVTL
 CJI-42.1 RTATNIWIDHNSFSNSSDGLVD
 CJI-42.2 KRTATNIWIDHNSFSNSSDGLVDK

CJI-43 KSMKVTVAFNQFGPNCGQRMPRARYGLHVANNNYD
 CJI-43.1 KSMKVTVAFNQFGPNCGQRMPRARYGLHV
 CJI-43.6 KSMKVTVAFNQFGPNSGQRMPRARYGLHV
 CJI-43.7 KSMKVTVAFNQFGPNCGQRMPRARYGLV
 CJI-43.8 KSMKVTVAFNQFGPNSGQRMPRARYGLV
 CJI-43.9 KSMKVTVAFNQFGPNCGQRMPRARYG
 CJI-43.10 KSMKVTVAFNQFGPNSGQRMPRARYG
 CJI-43.11 KSMKVTVAFNQFGPNSGQRMPRARYGKK
 CJI-43.12 KSMKVTVAFNQFGPNCGQRMPRARYG

CJI-45 PRARYGLHVANNNYDPWTIYAIGGSSNPT
 CJI-45.1 RARYGLHVANNNYDPWTIYAIGGSSNP
 CJI-45.2 RARYGLHVANNNYDPWTIYAIGGSS

CJI-44 DVFYNGAYFVSSGKYEGGNIYTKKEAFNVE
 CJI-44.1 NGAYFVSSGKYEGGNIYTKKEAFNVE
 CJI-44.2 NGAYFVSSGKYEGGNIYTKKEAFN
 CJI-44.3 KKNGAYFVSSGKYEGGNIYTKKEAFN

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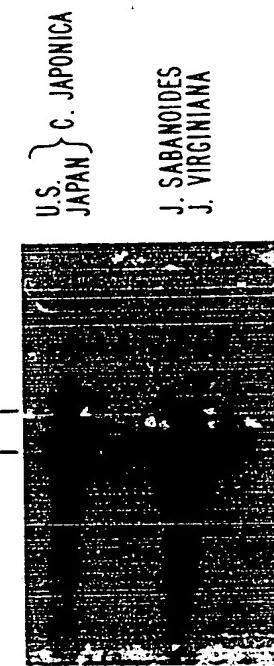


Fig. 19a

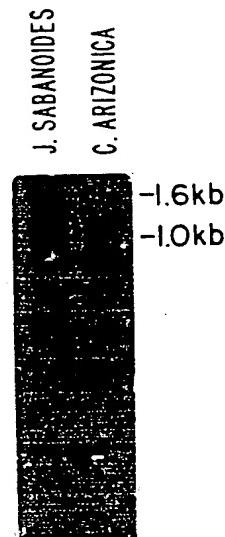


Fig. 19b

Fig. 20

CJI-42.5 DERTATNIWIDHNSFSNSSDD

CJI-42.8 DERTATNIWIDHNSFSNSSDGLAD

CJI-43.26 DEKSMKATVAFNQFGPNDE

CJI-43.27 DEKSMKVTAAPFNQFGPNDE

CJI-43.30 DEEKSMKATVAFNEFGPNDEE

CJI-43.31 DEEKSMKVTVAAANQFGPNDEE

CJI-43.32 DEEKSMKVTVAFNQAGPNDEE

CJI-43.35 DEKSMKATAAFNQFGPNDE

CJI-43.36 DEEKSMKATAAFNQFGPNDEE

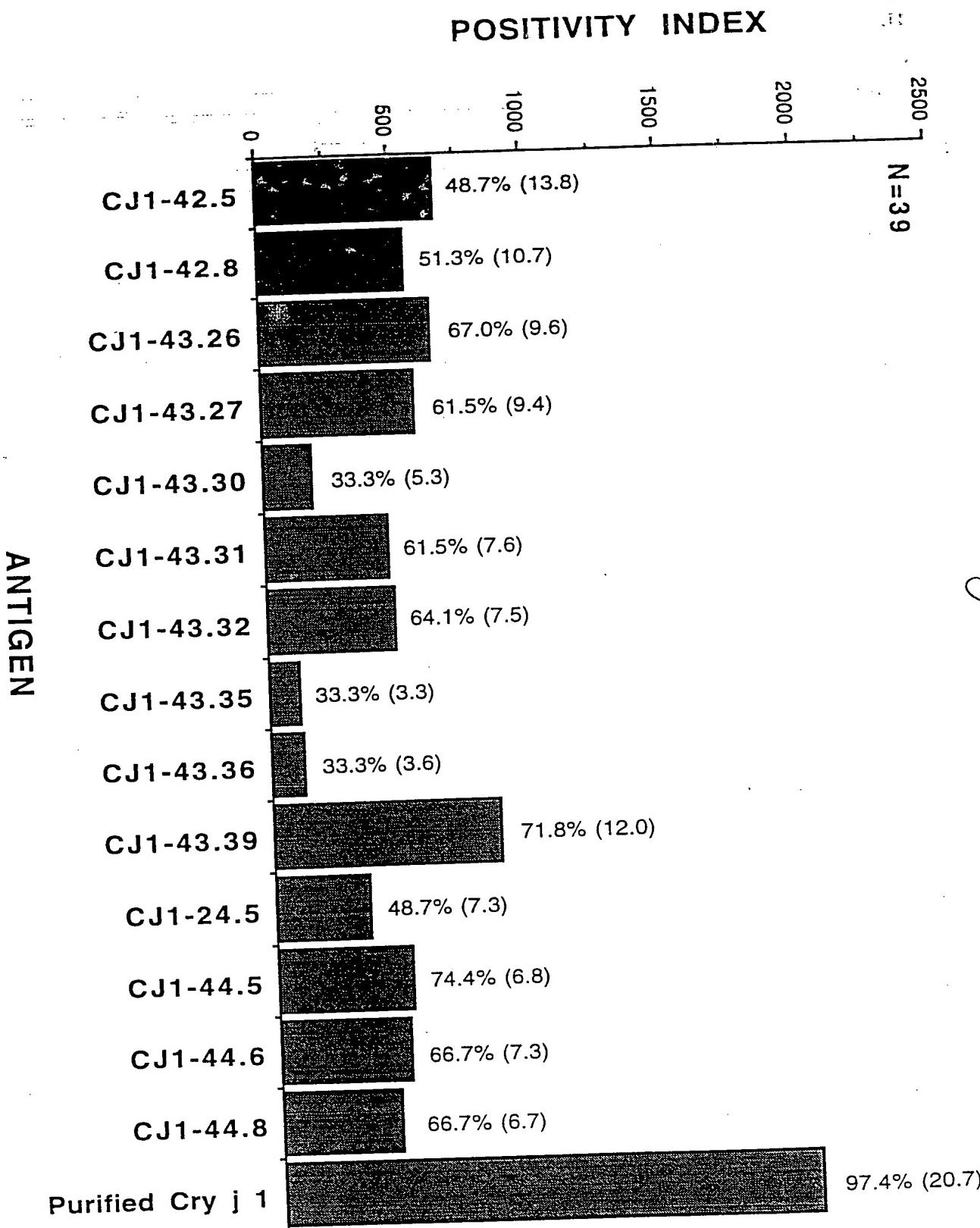
CJI-43.39 DDAYSDDKSMKVTVAFNQFGDE

CJI-24.5 DKEPRARYGLVHVANNYDPWTIEEE

CJI-44.5 DENGAYFVSSGKYEGGNIYTKKEAFNAE

CJI-44.6 DEENGAYFVSSGKYEGGNIYTKKEAFNVE

CJI-44.8 DEEGAYFVSSGKYEGGNIYTKKEAFNVE



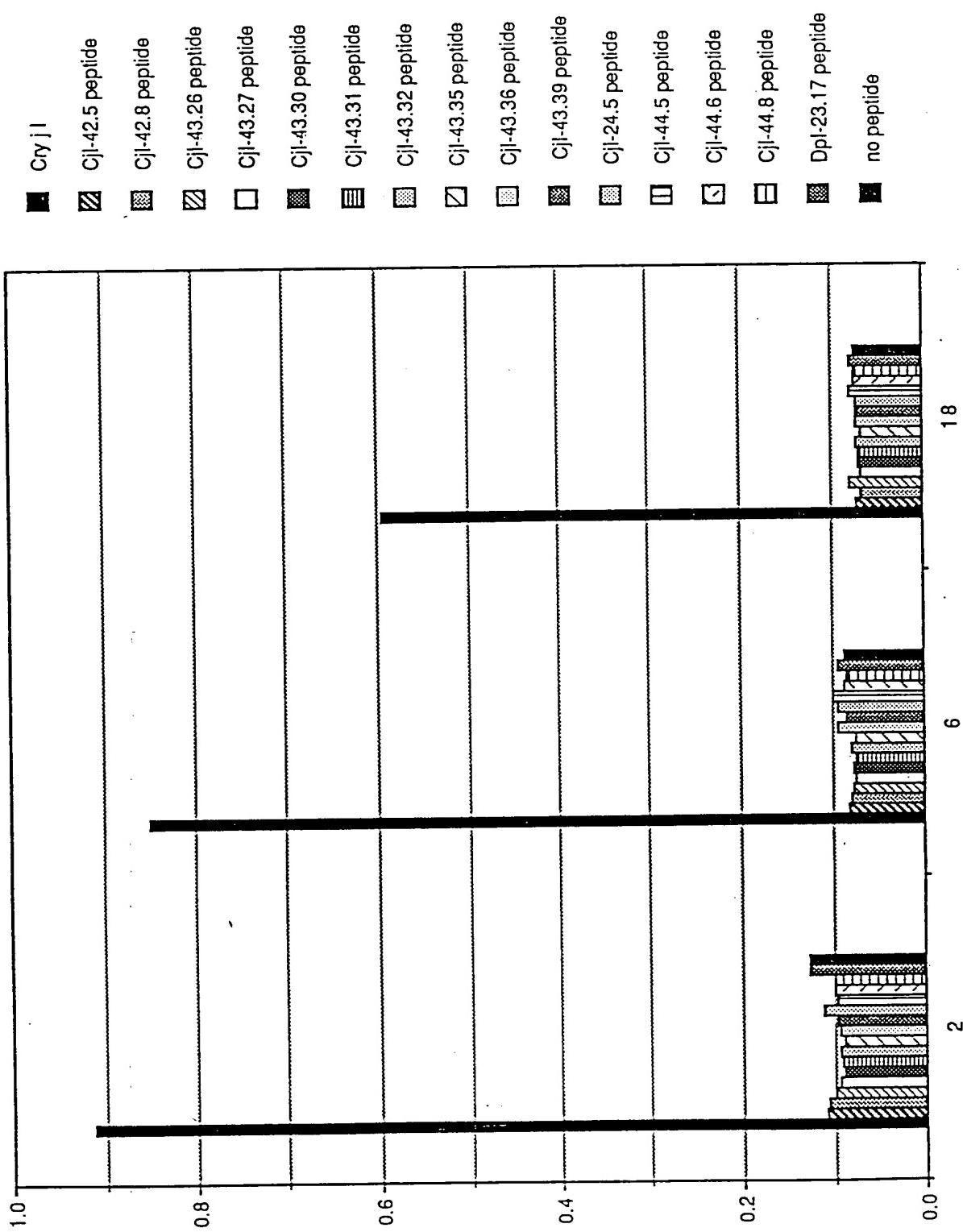


Fig. 22

1/dilution of plasma

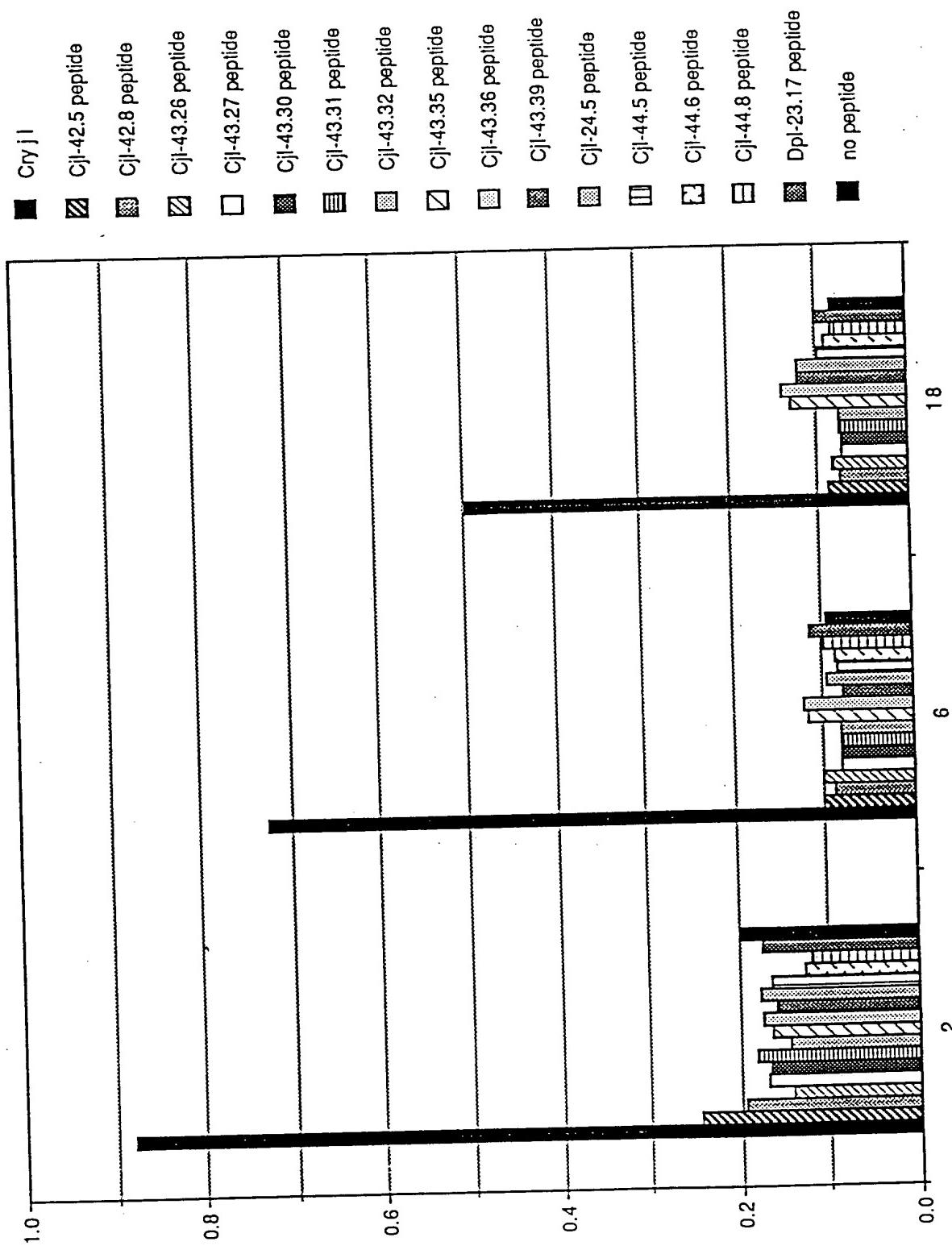


Fig. 23

1/dilution of plasma

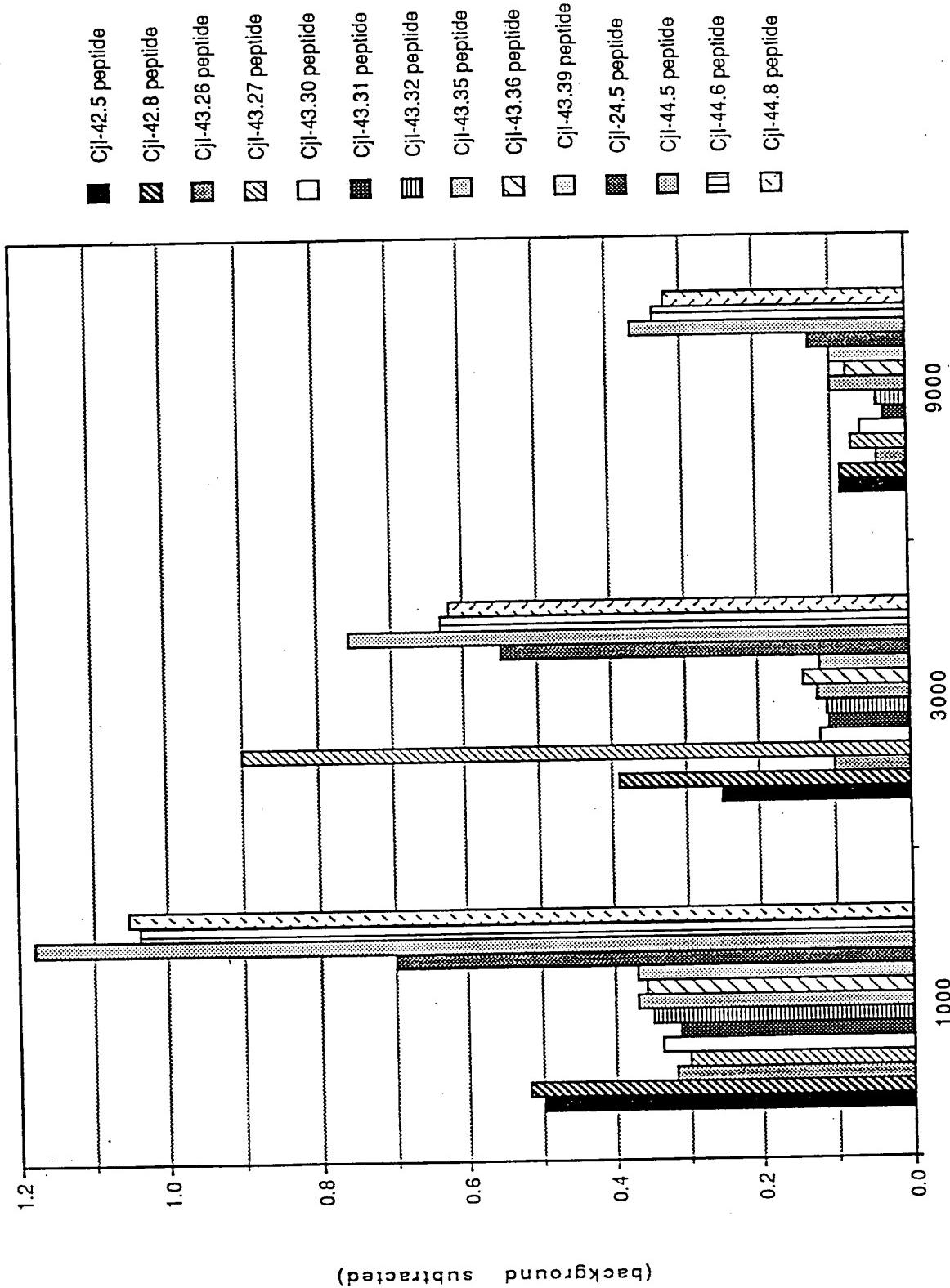


Fig. 24

1/dilution

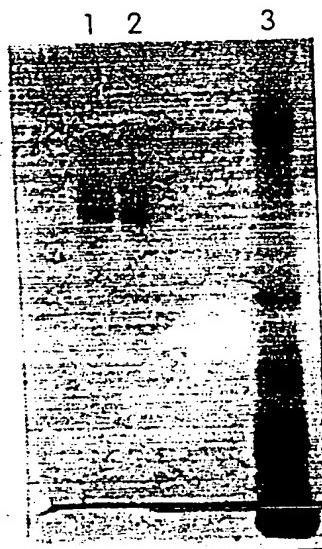


Fig. 25a

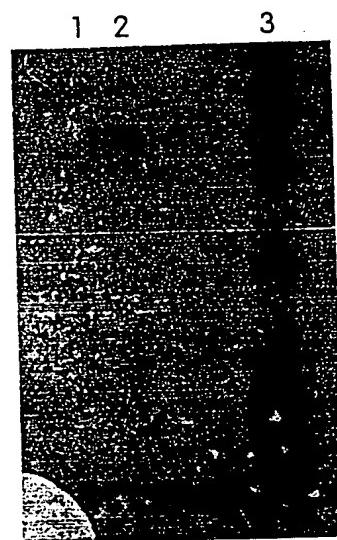


Fig. 25b

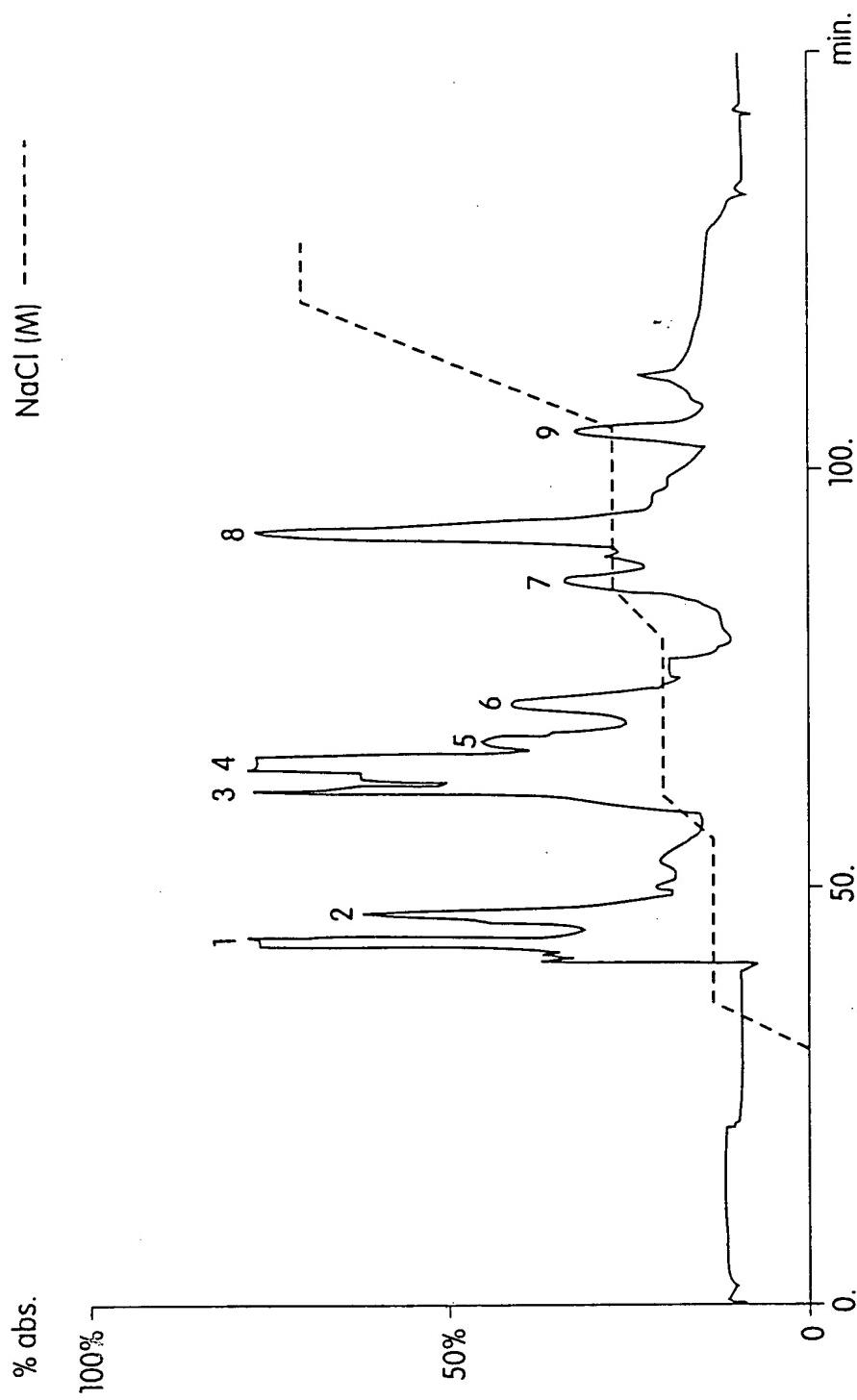


Fig. 26

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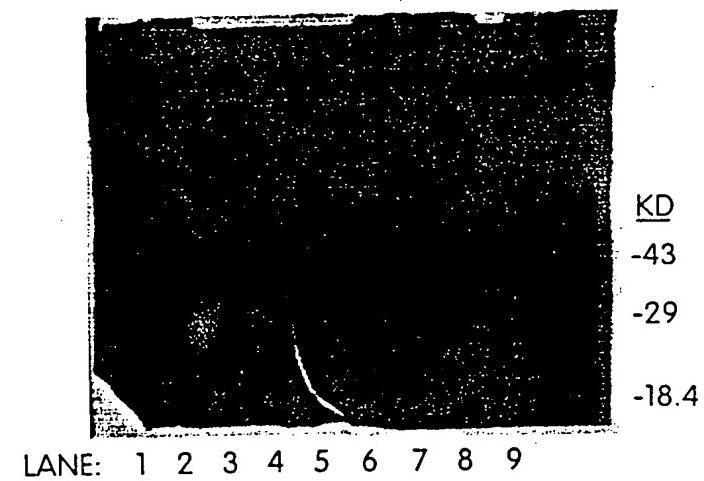


Fig. 27

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TGAGTTCGAGACAAGTATAGAAGAATTCTTTATTAAAATGGCCATGAAATTAAATTG
 M A M K L I

CTCCAATGGCCTTCTGCCCATGCAATTGATTATAATGGCGGCAGGAGAAGATCAATCTG
 A P M A F L A M Q L I I M A A E D Q S

CCCAAATTATGGACAGTGTGTCGAAAAATAATCTTAGATCGAATCGGAGTTAACGAA
 A Q I M L D S V V E K Y L R S N R S L R

AAGTTGAGCATTCTCGTCATGATGCTTCAACATCTTCAATGAAAGTATGGCGCAG
 K V E H S R H D A I N I F N V E K Y G A

Fig. 28.

250 260 270 280 290 300
 | | | | |
 TAGGCCATGGAAAGCATGATTGCACGTGAGGCATTTCACAGCATGGCAAGCTGCATGCAC
 V G D G K H D C T E A F S T A W Q A A C
 70 80
 310 320 330 340 350 360
 | | | | |
 AAAACCCATCAGCAAATGTTGCTTGTGCCAGGCAGCAAGAAATTGTGTGAAACAATCTGT
 K N P S A M L L V P G S K F V V N N L
 90 100
 370 380 390 400 410 420
 | | | | |
 TCTTCAATGGGCCATGTCACCTCACTTTACTTTAAGGTAGATAAGGATAATAAGCTGCGCT
 F F N G P C Q P H F T F K V D G I I A A A
 110 120
 430 440 450 460 470 480
 | | | | |
 ACCAAATCCAGGGAGCTGGAAAGAATAATAAGAATATGGTTGCAGTTTGCTAAACTTACAG
 Y Q N P A S W K N N R I W L Q F A K L T
 130 140

Fig. 28 Cont.

490 500 510 520 530 540
 | | | | |
 GTTTACTCTAAAGGGTAAAGGTGTAATTGATGGCAAGGAAACAAATGGTGGCTGGCC
 G F T L M G K G V I D G Q R W W A G
 150
 550 560 570 580 590 600
 | | | | |
 AATGTAATAATGGGTCAATGGACGGAGAAATTGCAACGATCGTGTAGACCAACAGGCCATTAA
 Q C K W V N G R E I C N D R P T A I
 170
 610 620 630 640 650 660
 | | | | |
 ATTTCGATTTCACGGGTCTGATAATCCAAGGACTGAAACTAATGAACAGTGCCCCGAAT
 K F D F S T G L I I Q G L K L M N S P E
 190
 670 680 690 700 710 720
 | | | | |
 TTCAATTAGTTTGGGAATTGTGAGGGAGTAAATCATGGCATTAGTATTACGGCAC
 F H L V F G N C E G V K I I G I S I T A
 210

Fig 28 Cont.

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730	740	750	760	770	780
CGAGGACAGTCCCTAACACTGATGGATTGATA	TCTTGCATCTAA	AAACTTTCACTTAC			
P R D S P N T D G I D I F A S K N F H L					
230	240				
790	800	810	820	830	840
AAAAGAACACGGATAGGAACACGGGATGACTGCGTCCGCTATA	GGCACAGGGTCTTCTTAATA				
Q K N T I G T D C V A I G T G S S N					
250	260				
850	860	870	880	890	900
TTGTGATTGAGGATCTGATTTCGGGTCCAGGCCATGGAATAAGTATA	GGAAAGTCTTGGGA				
I V T E D L I C G P G H G I S I G S L G					
270	280				
910	920	930	940	950	960
GGGAAACTTAGGAGGTTCACTACGTGCACGTTAAATTCA	TAGACA				
R E N S R A E V S Y V H V N G A K F I D					
290	300				

Fig.28 Cont.

970 980 990 1000 1010 1020
 | | | | |
 CACAAAATGGATTAAAGAATCAAACATGGCAGGGTGGTTCAAGGCATGGCAAGCCATATAA
 T Q N G L R I K T W Q G G S G M A S H I
 310 320
 1030 1040 1050 1060 1070 1080
 | | | | |
 TTTATGAGAAATGTTGAATGATAAAATTGGAGAACCCCCATATTAAATAATCAATTCTACT
 I Y E N V E M I N S E N P I L I N Q F Y
 330 340
 1090 1100 1110 1120 1130 1140
 | | | | |
 GCACACTCAGCTTCTGCTTGCCAAACCAACCAGAGGGTCCTGGGTCAAATCCAAGATGGACAT
 C T S A S A C Q N Q R S A V Q I Q D V T
 350 360
 1150 1160 1170 1180 1190 1200
 | | | |
 ACAAGAACATACGTTGGGACATCAGCAACAGCAGCAATTCAACTTAAGTGCAGTGACA
 Y K N I R G T S A T A A I Q L K C S D
 370 380

Fig. 28 Cont.

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Fig. 28 Cont.

1450 1460 1470 1480 1490 1500
 | | | | |
 GGTCGAGGCCCTCCGAATTGTACAAACAAATGTCATGGTTGCAGTCCATGTAAGGCCAAGT
 G S R P P N C T N K C H G C S P C K A K
 470 480

1510 1520 1530 1540 1550 1560
 | | | | |
 TAGTTATTGTTCATCGTATTATGCCGGCAGGAGTATTATCCTCAGAGGTGGATATGCAGGCT
 L V I V H R I M P Q E Y Y P Q R W I C S
 490 500

1570 1580 1590 1600 1610 1620
 | | | | |
 GTCATGGCAAATCTACCATAATGAGATAACATTGAAACTGTATGTGCTAGTGAATA
 C H G K I Y H P -
 510 514

1630 1640 1650 1660 1670 1680
 | | | |
 TTCTTGTGGTACAATATTGAAACTGATATTGAAATAATCATCAATGTTCTAAGGCAT

1690 1700 1710 1720
 | | |
 TTATAATAGATTATAATTGTTCAAGCCTGGTGCAAAAAAAAAA

Fig. 28 Cont.

10	20	30	40	50
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLD SVVEKYLRSNRSLRKVEH				
60	70	80	90	100
SRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKK				
110	120	130	140	150
FVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTL				
160	170	180	190	200
MGKGVIDGQGKQWWAGQCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLK				
210	220	230	240	250
LMNSPEFH LVFGNCEGVKIIGISITAPRDSPNTDGIDIFASKNFHLQKNT				
260	270	280	290	300
IGTGDDCVAIGTGSSNIVIEDLICPGHGSI SIGSLGRENSRAEVSYVHVN				
310	320	330	340	350
GAKFIDTQNGLRIKTWQGGSGMASHIIYENVEMINSEN PILINQFYCTSA				
360	370	380	390	400
SACQNQRSAVQIQDV TYKNIRGT SATAAAIQLKCSDSMPCKDIKLSDISL				
410	420	430	440	450
KLTSGKIASCLNDNANGYFSGHVIPACKNLSPSAKRKESKSHKHPKTVMV				
460	470	480	490	500
ENMRAYDKGNRTRILLGSRPPNCTNKCHGCSPCKAKLVIVHRIMPQEYYP				
510	514			
QRWICCSCHGK IYHP				

Fig. 29

Cry j II	50	R K V E H S R H D A T N I F N V E K Y G A	60	S R H D A T N I F N V E K Y G A
LONG		R K V E H S R H D A T N I F N V E K Y G A		
SHORT		S R H D A T N I F N V E K Y G A		
SAKAGUCHI		A I N I F N V E K Y		
Cry j II	70	V G D G K H D C T E A F S T A W Q A A C K N P S	80	V G D G K H D C T E A F S T A W(Q))K N P()
LONG		V G D G K H D C T E A F S T A W(Q))K N P()		
SHORT		V G D G K H D C T E A F S T A W(Q))X N P()		

Fig 30

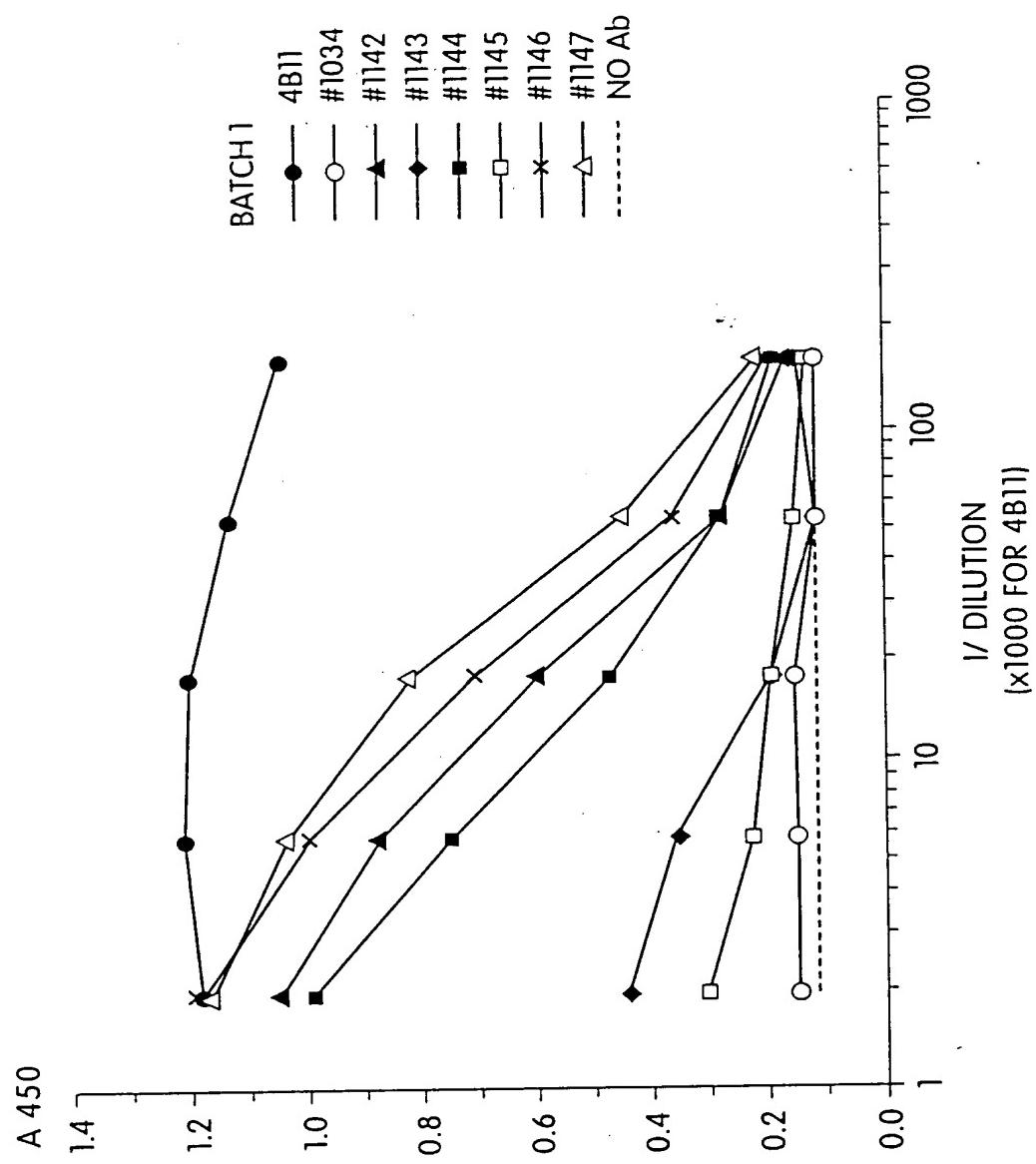


Fig. 31

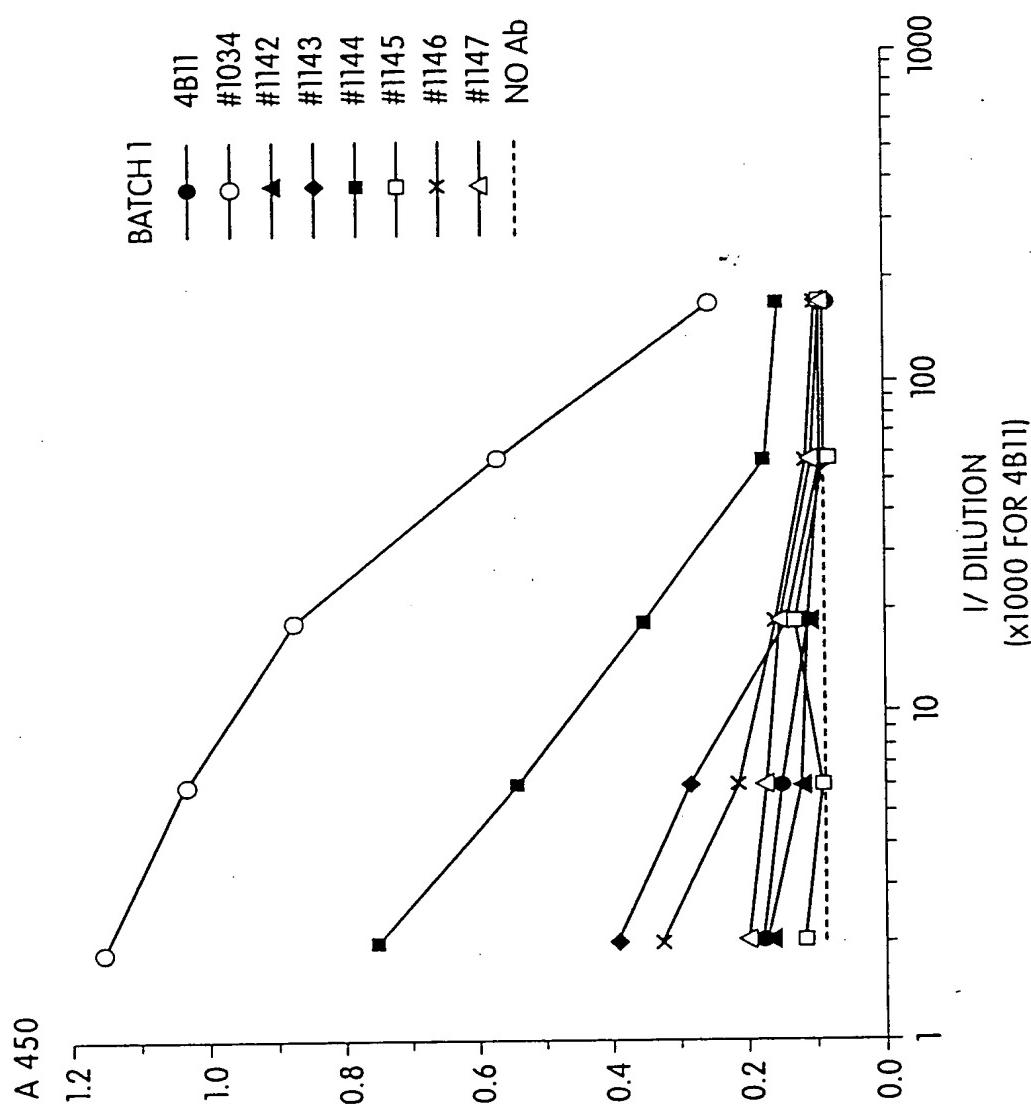


Fig. 32

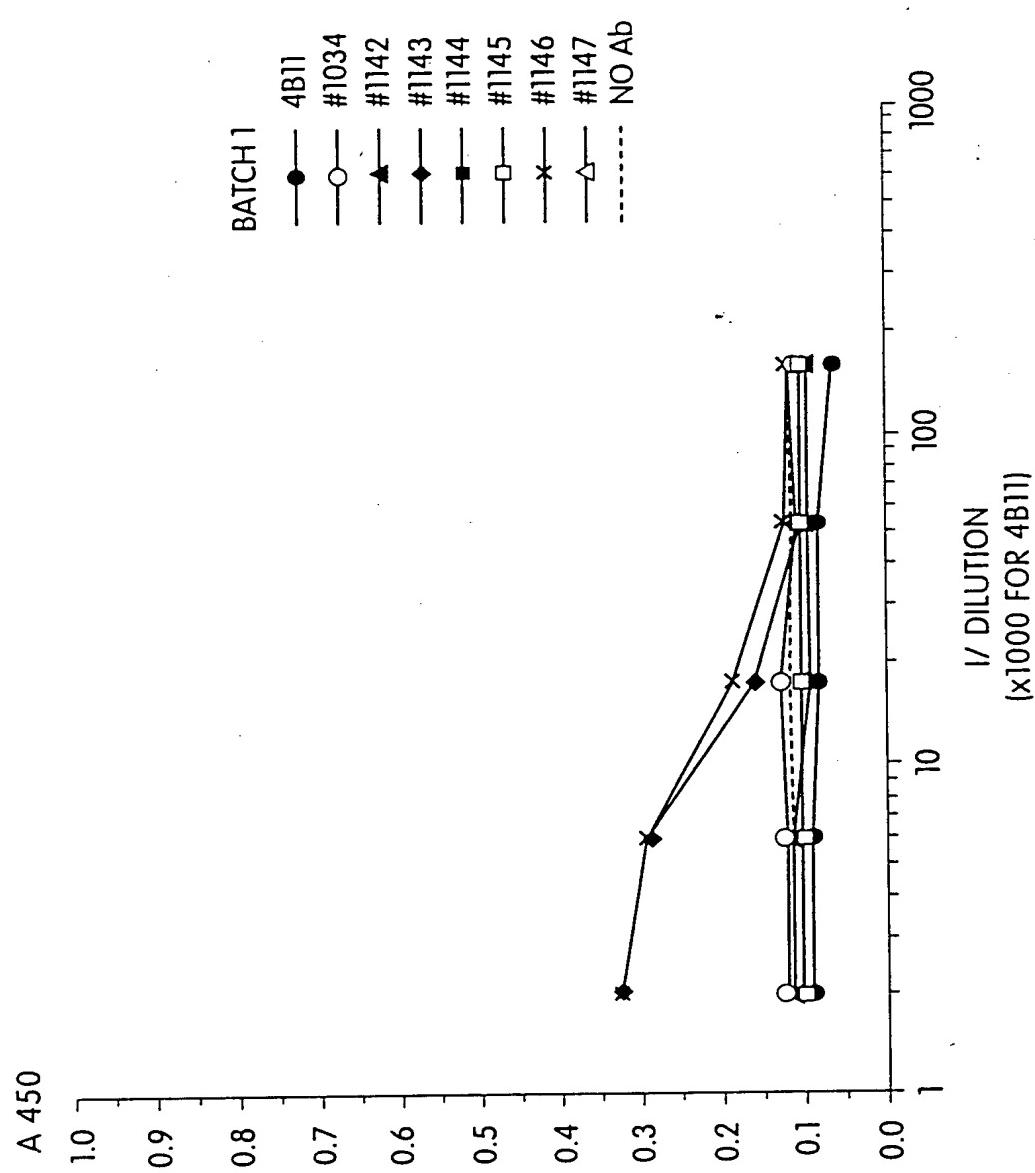


Fig. 33

08/226248

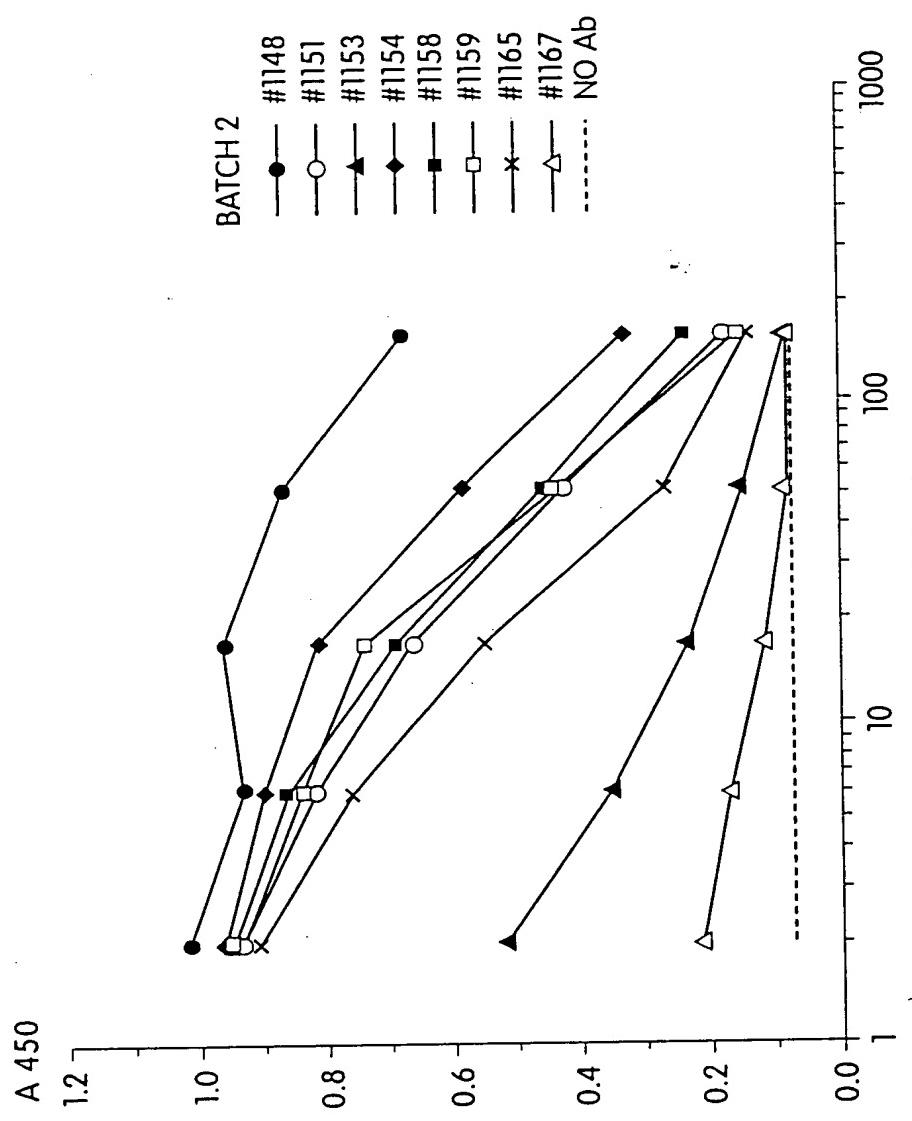


Fig. 34

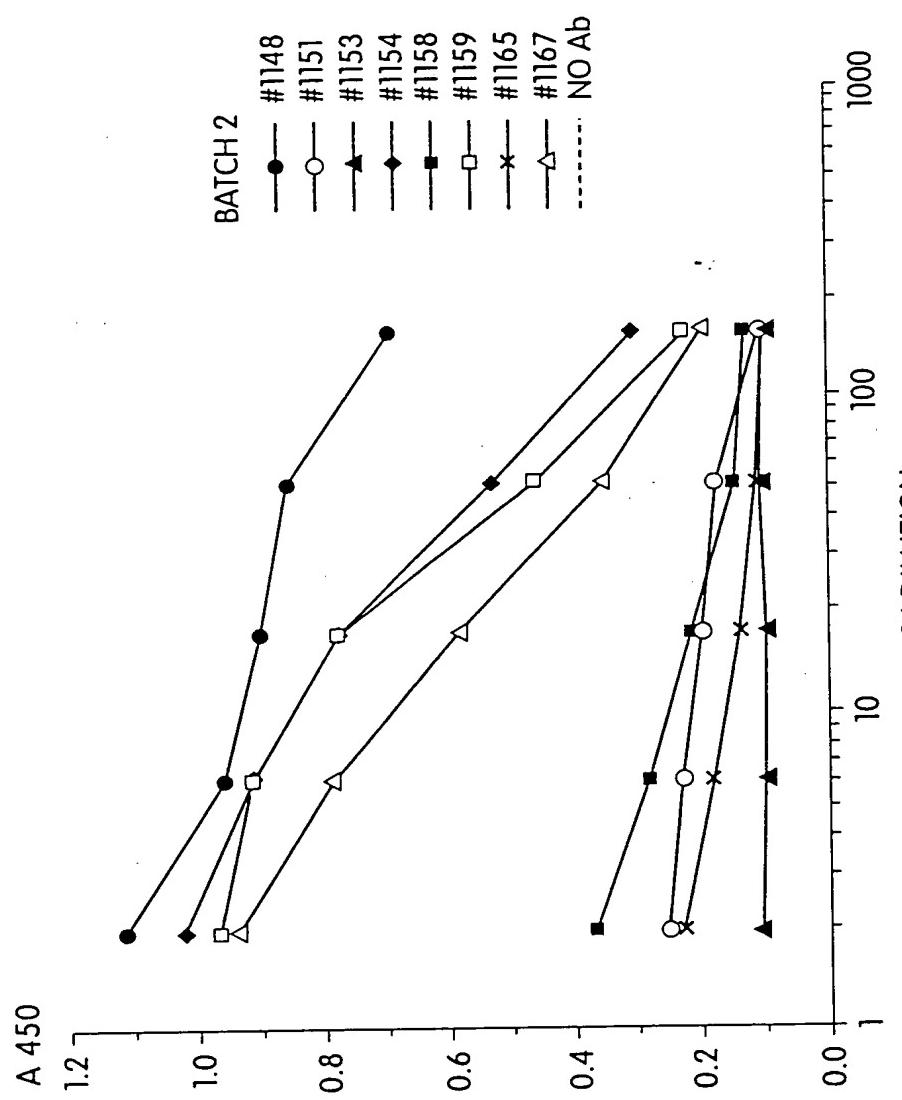


Fig. 35

08/226248

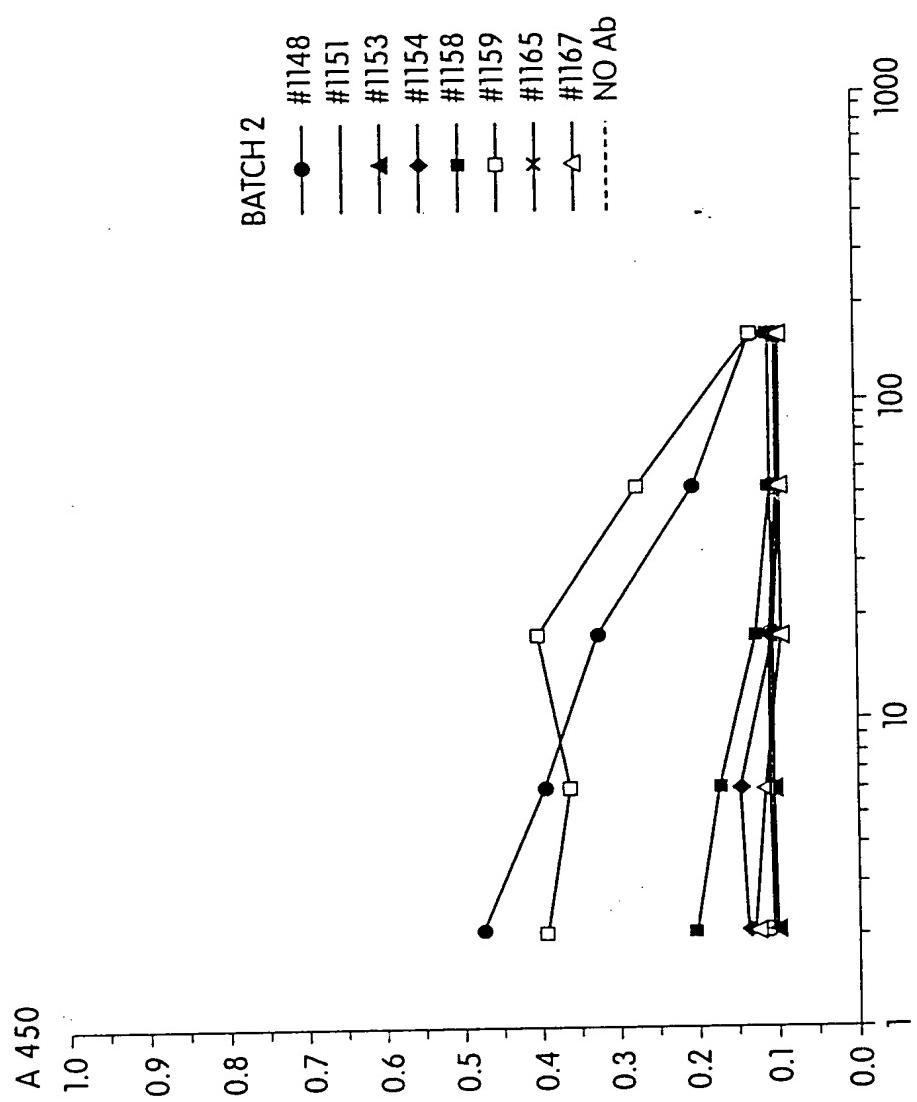


Fig. 36

08/226248

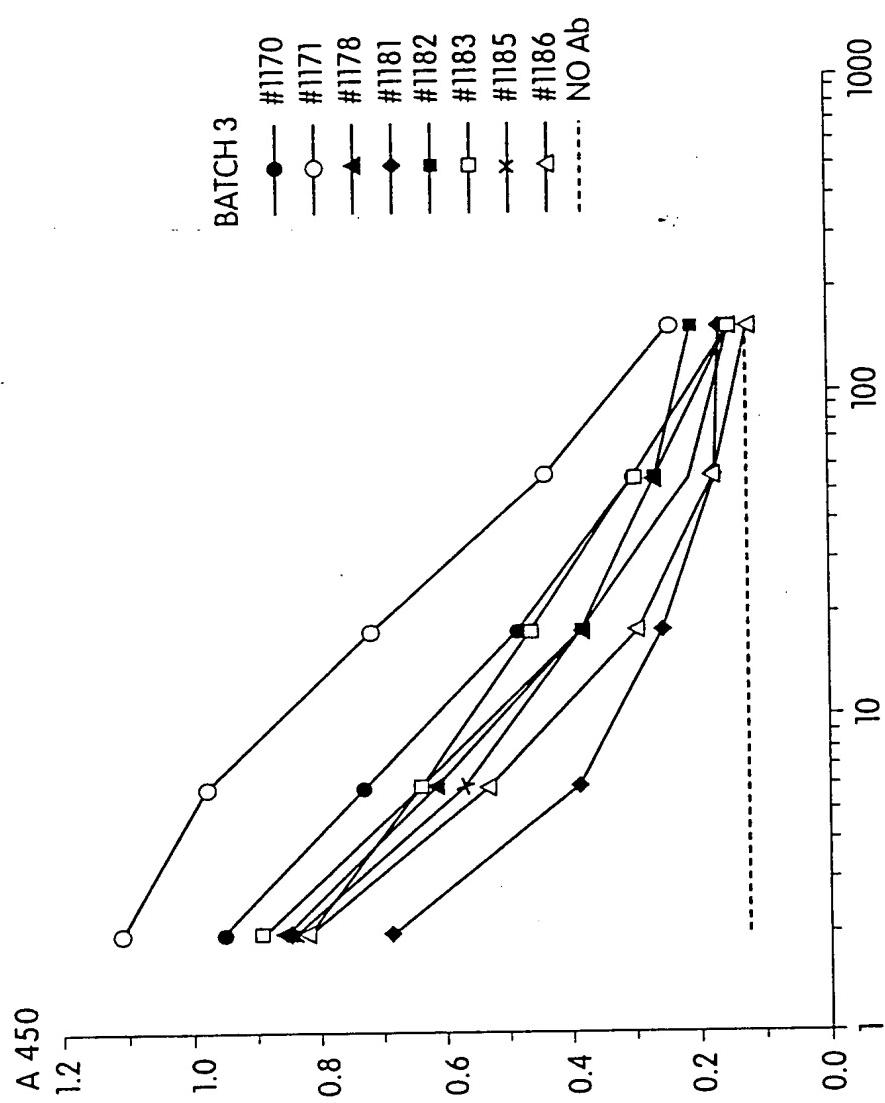


Fig. 37

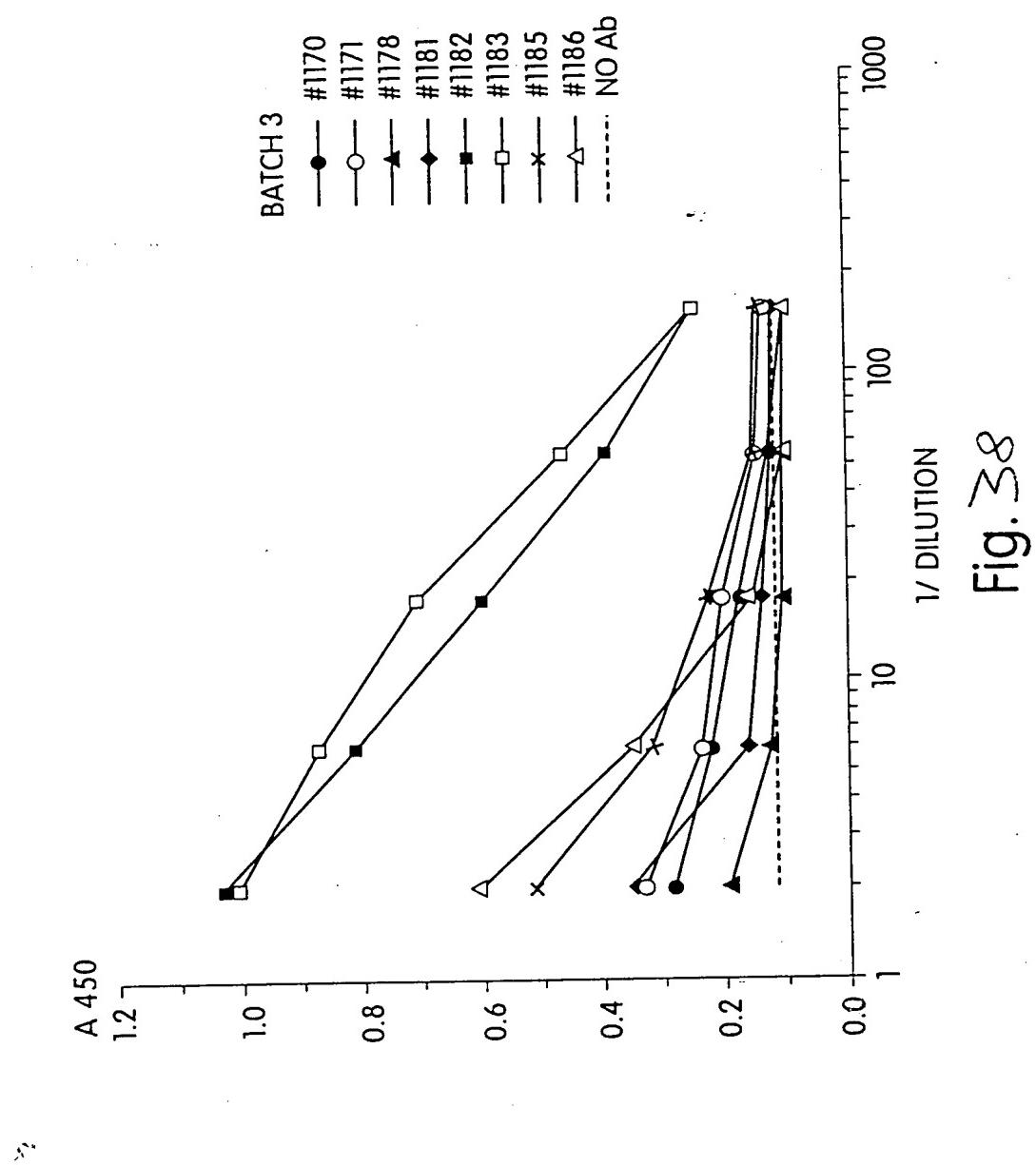


Fig. 38

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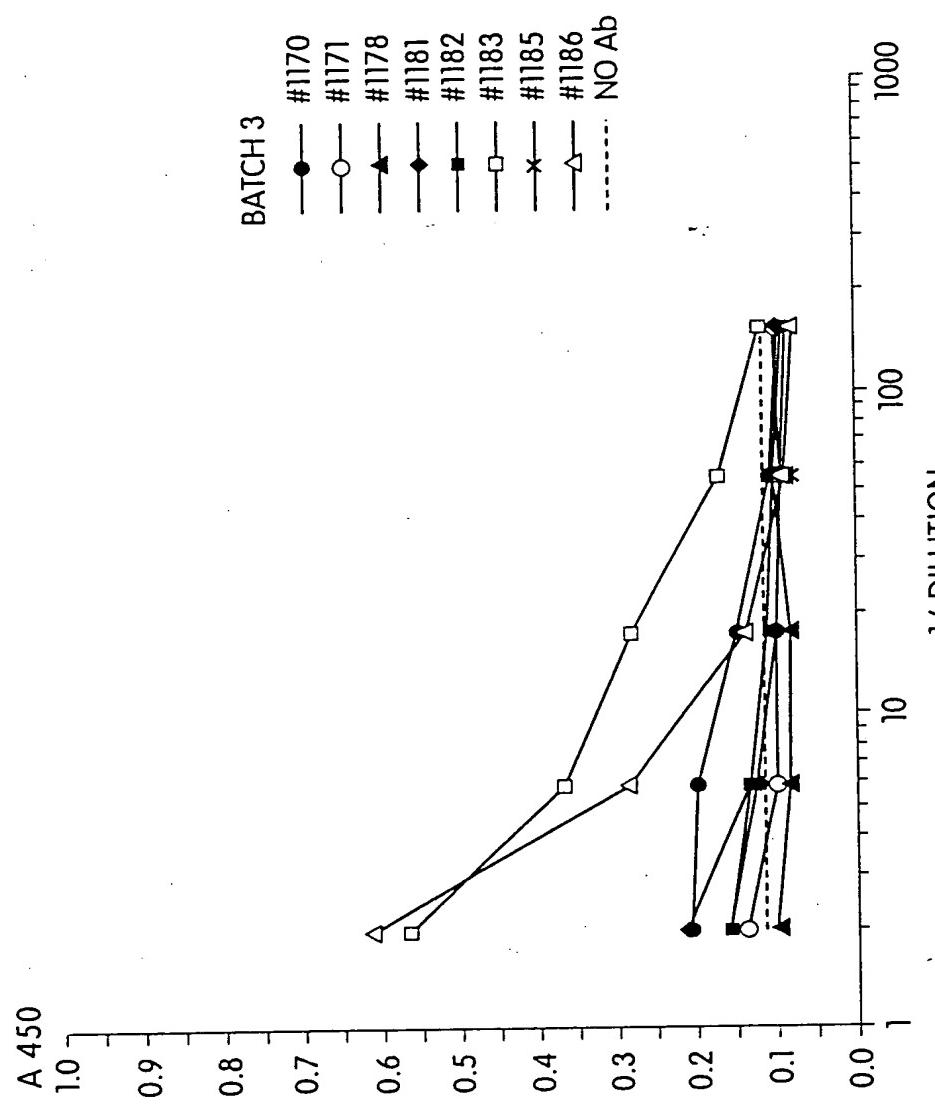


Fig. 39

PATIENT #	MAST	PURIFIED NATIVE Cry j II	PURIFIED NATIVE Cry j II	RECOMBINANT Cry j II (rCry j II)
1034	2	-	+	-
1142	2	+	-	-
1143	0	+	+	+
1144	1	+	+	-
1145	0	-	-	+
1146	3	+	-	-
1147	3	+	-	-
1148	3	+	+	+
1151	3	+	+	-
1153	1	+	-	-
1154	3	+	+	-
1158	2	+	+	-
1159	2	+	+	+
1165	1	+	-	+
1167	1/0	-	+	-
1170	1/0	+	-	-
1171	2	+	-	-
1178	1	+	-	-
1181	1/0	+	-	-
1182	1	+	+	-
1183	1	+	+	+
1185	1/0	+	+	-
1186	1/0	+	+	+
POSITIVE	21	20	13	5

Fig. 40

FIG. 41

Cry j IIA

FTFKVDGIIAAAYQ

Cry j II B

NGYFSGHVIPACKN

Cry j II C:

1	10	20	30	40	50	60	
MGHHHHHH	HEFRKVEHSRHD	AINIFNVEKYGA	AVGDGKHDC	TEAFSTAWQAAC	KNPSAMLLV		
70	80	90	100	110	120		
PGSKKFVVNNLFFNNGPCQPHFTFKVDGI	IAAYQNPASWKNR	IWLQFAKL	TGFTLMGKG	V			
128							
IDGQGKQW							

Cry j III D:

1	10	20	30	40	50	60	
MGHHHHHH	HEFWAGQCKWVNGREICNDRDRPTAIKFDFSTGLIIQGL	KLMNSPEFH	LVFGN				
70	80	90	100	110	120		
CEGVKIIGISITAPRDSPNTDGIDIFASKNFHLQKNTIGTGDDCVA	IGTGSSNIVIEDLI						
127							
CGPGHGI							

Fig. 41 Cont.

Cry j III:

1 10 20 30 40 50 60
 | | | | | | |
 MGHHHHHHEFSIGSLGRENSRAEVSYVHVNGAKFIDTQNGLRIKTWQGGSGMASHIYEN
 70 80 90 100 110 120
 | | | | | |
 VEMINSEN PILIN QFYCTSASACQNQRSAVQIQDVTYKNIRGTSATAAAIQLKCSDSMPC
 127
 |
 KDIKLSD

Cry j III:

1 10 20 30 40 50 60
 | | | | | | |
 MGHHHHHHEFISLKLTSKGKIASCLNDNANGYFSGHVIPACKNLSPSAKRKESKSHKHPKT
 70 80 90 100 110 120
 | | | | | |
 VMVENMRAYDKGNRTRILLGSRPPNCTNKCHGSPCKAKLVIVHRIMPQEYYPQRWICSC
 127
 |
 HGKIYHP

Cry j IIG (J1) GKGVIDGQGKQWWAGQCKWVNGRE

Cry j-IIH (J3) DSMPCKDIKLSDISLKLTSGKIAS

Cry j-IIQ (J2) IEDLICGPGHGISISIGSLGRENSRA

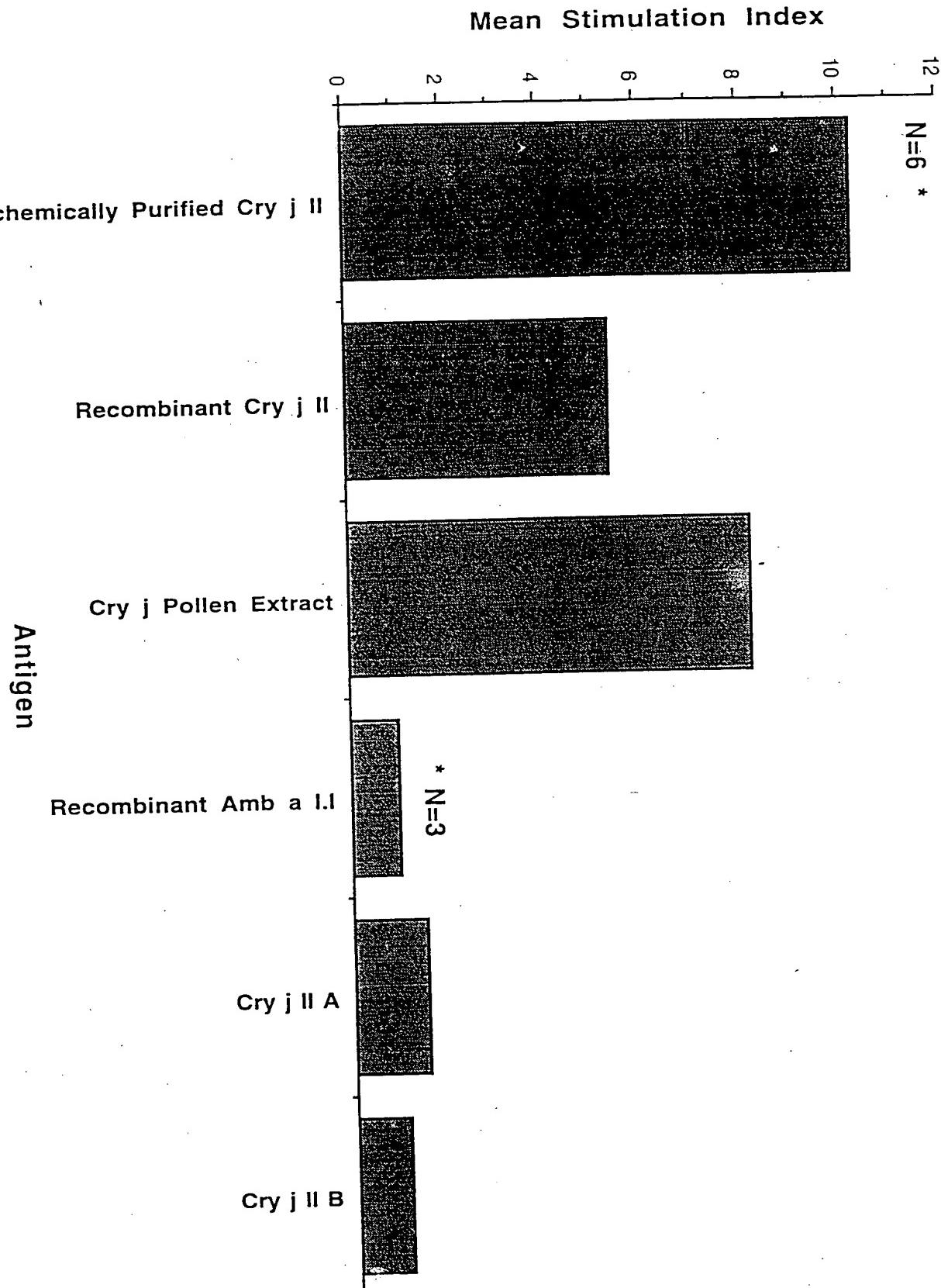


Fig 42

08/226248

Fig. H3

